



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number 194838

TO: Chun Crowder  
Art Unit: 1644  
Location: REM-3B59&3C70  
Serial Number: 1009809

Thursday, July 20, 2006

From: Beverly Shears  
Location: Biotech-Chem Library  
REM 1A54  
Phone: 571-272-2528  
[beverly.shears@uspto.gov](mailto:beverly.shears@uspto.gov)

### Search Notes

Your queries have completed processing. You may access an electronic version via eDAN (SCORE) and /or <http://es/ScoreAccessWeb>. If the result files have been separated into two (2) or more versions, you may view additional files via the select "[View version list for this application](#)" link.

#### Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

#### Published Applications Database - November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).



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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:50:22 ; Search time 40.6452 Seconds  
(without alignments)  
112.490 Million cell updates/sec

Title: US-10-009-809-1

Perfect score: 57

Sequence: 1 KNNLKECGLY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A\_Geneseq.8.\*

1: Geneseq.1980s.\*

2: Geneseq.1990s.\*

3: Geneseq.2000s.\*

4: Geneseq.2001s.\*

5: Geneseq.2002s.\*

6: Geneseq.2003as.\*

7: Geneseq.2003bs.\*

8: Geneseq.2004s.\*

9: Geneseq.2005s.\*

10: Geneseq.2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	57	100.0	10	5	Aae26131 Galphai3
2	57	100.0	10	5	Aae26129 Galphai3
3	57	100.0	11	6	Abj36694 G protein
4	57	100.0	11	7	Abw00024 Human G a
5	57	100.0	11	7	Adf45287 Human G a
6	57	100.0	11	8	Adt51095 G protein
7	57	100.0	13	7	Abw00012 Human G a
8	57	100.0	13	7	Adf45266 G alpha c
9	57	100.0	25	4	Aay72138 Anti-alle
10	57	100.0	25	5	Aae26149 Galphai3
11	57	100.0	25	5	Aae26157 Peptide u
12	57	100.0	26	4	Aay72140 Anti-alle
13	57	100.0	26	4	Aay72151 Succinyla
14	57	100.0	26	4	Aay72153 Anti-alle
15	57	100.0	26	4	Aay72139 Anti-alle
16	57	100.0	26	5	Aae26158 Galphai3
17	57	100.0	26	5	Aae26139 Galphai3
18	57	100.0	26	5	Aae26140 Galphai3
19	57	100.0	26	5	Aae26147 Galphai3
20	57	100.0	26	5	Aae26154 Peptide 2
21	57	100.0	26	5	Aae26156 Peptide 2
22	57	100.0	27	4	Aay72146 Anti-alle
23	57	100.0	27	4	Aay72150 N-termina

24	57	100.0	353	7	ADD46015
25	57	100.0	354	3	Aay94207 Rat Prote
26	57	100.0	354	4	Abg99066 Human G-p
27	57	100.0	354	5	Abb09275 G protein
28	57	100.0	354	7	Adc09610 Human G-p
29	57	100.0	354	7	Adi62697 Human apo
30	57	100.0	354	8	Adu60729 Human G-p
31	52	91.2	10	5	Aae26134 Anti-alle
32	52	91.2	26	5	Aae26141 Galphai3
33	51	89.5	10	5	Aae26133 Anti-alle
34	51	89.5	10	5	Aae26136 Anti-alle
35	51	89.5	26	5	Aae26142 Galphai3
36	51	89.5	26	5	Aae26145 Galphai3
37	51	89.5	26	5	Aae26137 Galphai3
38	50	87.7	10	2	Aar61259 Control p
39	50	87.7	10	2	Aar49785 Farnesylt
40	50	87.7	10	2	Aaw04476 Weak inh
41	50	87.7	10	5	Aae26132 Anti-alle
42	50	87.7	10	5	Aae26151 Galphai2
43	50	87.7	11	6	Abj36692 G protein
44	50	87.7	11	8	Adt51091 G protein
45	50	87.7	13	6	Abj36771 G protein
46	50	87.7	13	7	Abw00010 Human G a
47	50	87.7	13	7	Adf45264 G alpha c
48	50	87.7	13	8	Adt51186 G protein
49	50	87.7	23	4	AAO08372 Human pol
50	50	87.7	26	4	Aay72144 Modified
51	50	87.7	26	5	Aae26144 Galphai3
52	50	87.7	26	5	Aae26148 Galphai3
53	50	87.7	27	4	Aay72145 Anti-alle
54	50	87.7	288	6	AbR41313 Human DIT
55	50	87.7	339	7	Adm05136 Human pro
56	50	87.7	339	7	Adm04957 Human pro
57	50	87.7	339	9	Aec87887 Human CDN
58	50	87.7	339	9	Aec88066 Human CDN
59	50	87.7	353	7	AdE57521 Human Pro
60	50	87.7	353	7	AdE57515 Rat Prote
61	50	87.7	353	7	AdE57517 Human Pro
62	50	87.7	353	7	AdE57519 Rat Prote
63	50	87.7	353	8	Adn06152 Rat Gil-H
64	50	87.7	354	3	Aay85290 Human G-a
65	50	87.7	354	4	Aab99064 Human G-p
66	50	87.7	354	5	AbB09273 G protein
67	50	87.7	354	7	AbR82632 C. elegan
68	50	87.7	354	7	AdC09608 Human G-p
69	50	87.7	354	7	AdE59387 Human Pro
70	50	87.7	354	7	AdE59391 Human Pro
71	50	87.7	354	7	AdE59385 Rat Prote
72	50	87.7	354	7	AdE59389 Rat Prote
73	50	87.7	354	7	AdD46017 Human Pro
74	50	87.7	354	8	Adn06138 Rat Gil a
75	50	87.7	354	8	AdQ08808 Ciona int
76	50	87.7	354	8	AdU60727 Human G-p
77	50	87.7	354	8	AdY16245 PRO poly
78	50	87.7	355	3	Aay85149 Human G-a
79	50	87.7	355	3	Aay89065 Human G-p
80	50	87.7	355	5	Abb09274 G protein
81	50	87.7	355	5	AbB09277 G protein
82	50	87.7	355	5	Aau79335 Human inh
83	50	87.7	355	7	AdC09612 Human G-p
84	50	87.7	355	7	AdC09609 Human G-p
85	50	87.7	355	7	AdJ68621 Human hea
86	50	87.7	355	7	AdJ70586 Human hea
87	50	87.7	355	7	AdP70781 Minicell
88	50	87.7	355	8	Adm67196 Human adi
89	50	87.7	355	8	Abm80456 Tumour-as
90	50	87.7	355	8	AdU60731 Human G-p
91	50	87.7	355	8	AdU60728 Human G-p
92	50	87.7	355	9	AdX06906 Cyclin-de
93	50	87.7	362	8	AdG36979 Human GPC
94	50	87.7	408	9	Aed74272 Human pla
95	50	87.7	695	6	AbR56305 pc901HISG
96	50	87.7	709	4	AbB56396 TSHR-Gs-a

97 50 87.7 709 6 ABR55447 Abr55447 Amino aci  
98 50 87.7 709 8 ADU24238 Adu24238 Human MHC  
99 50 87.7 725 4 AAB99036 Aab99036 Human som  
100 50 87.7 784 7 ADG37260 Adg37260 Fusion co

## ALIGNMENTS

RESULT 1  
AAE26131  
ID AAE26131 standard; peptide; 10 AA.  
XX  
AC AAE26131;  
XX  
DT 14-NOV-2002 (first entry)  
XX  
DE Galphai3 cyclic peptide.  
XX  
KW Antiallergic agent; nasal allergy; eye; skin; acute urticaria; psoriasis;  
KW psychogenic; allergic asthma; interstitial cystitis; bowel disease;  
KW multiple sclerosis; dermatological; antiinflammatory; neuroprotective;  
KW migraine; cyclic.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /note= "This residue is linked to Tyr at position 10 by  
FT epsilon-NH"  
FT  
FT Misc-difference 10 /note= "This residue is linked to Lys at position 1 by  
FT epsilon-NH"  
FT  
XX WO200250097-A2.  
XX  
XX 27-JUN-2002.  
XX  
XX 20-DEC-2001; 2001WO-IL001186.  
XX  
XX 21-DEC-2000; 2000IL-00140473.  
XX  
XX (ALLE-) ALLERGENE LTD.  
XX  
XX Eisenberg R, Raz T;  
XX  
XX WPI; 2002-636474/68.  
XX  
XX New antiallergic agent having first cell penetrating segment joined to  
XX antiallergic decapeptide providing antiallergic effect within mast cells,  
XX through linker which provides bend or turn at junction between segments.  
XX  
XX Claim 8; Page 57; 81pp; English.  
XX  
XX The invention relates to an antiallergic agent, comprising a complex  
XX molecule having at least a first segment competent for importation of the  
XX molecule into mast cells, joined to a second segment through a linker,  
XX where the second segment is the anti-allergic decapeptide derived from  
XX Galphai 3, providing antiallergic effect within mast cells, and linker  
XX provides a bend or turn at or near junction between the two segments. The  
XX invention is useful for treating allergic conditions such as nasal  
XX allergy, allergic reactions in an eye of the subject, allergic reactions  
XX in the skin of the subject, acute urticaria, psoriasis, psychogenic or  
XX allergic asthma, interstitial cystitis, bowel diseases, migraines or  
XX multiple sclerosis. The invention is also useful for preventing late  
XX phase inflammatory responses induced by protein kinase activation,  
XX preferably mitogen activated protein kinase activation, where the  
XX antiallergic agent is peptide 2, peptide 2-Succ and peptide 2-Cyc. The  
XX invention provides specific direct and targeted treatment of allergies  
XX and related inflammatory conditions. The present sequence is Galphai3  
XX cyclic peptide  
XX Sequence 10 AA;

Query Match 100.0%; Score 57; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00099;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKECGLY 10  
Db 1 KNNLKECGLY 10  
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RESULT 2  
AAE26129  
ID AAE26129 standard; peptide; 10 AA.  
XX

AC AAE26129;  
XX  
DT 14-NOV-2002 (first entry)  
XX  
DE Galphai3 decapeptide.

XX Antiallergic agent; nasal allergy; eye; skin; acute urticaria; psoriasis;  
KW psychogenic; allergic asthma; interstitial cystitis; bowel disease;  
KW multiple sclerosis; dermatological; antiinflammatory; neuroprotective;  
KW migraine.  
XX  
OS Unidentified.

XX  
XX WO200250097-A2.  
XX  
XX 27-JUN-2002.  
XX

PF 20-DEC-2001; 2001WO-IL001186.  
XX  
XX 21-DEC-2000; 2000IL-00140473.  
XX  
XX (ALLE-) ALLERGENE LTD.  
XX

PI Eisenberg R, Raz T;  
XX  
XX WPI; 2002-636474/68.  
XX  
XX New antiallergic agent having first cell penetrating segment joined to  
XX antiallergic decapeptide providing antiallergic effect within mast cells,  
XX through linker which provides bend or turn at junction between segments.  
XX

XX Claim 8; Page 57; 81pp; English.  
XX  
XX The invention relates to an antiallergic agent, comprising a complex  
XX molecule having at least a first segment competent for importation of the  
XX molecule into mast cells, joined to a second segment through a linker,  
XX where the second segment is the anti-allergic decapeptide derived from  
XX Galphai 3, providing antiallergic effect within mast cells, and linker  
XX provides a bend or turn at or near junction between the two segments. The  
XX invention is useful for treating allergic conditions such as nasal  
XX allergy, allergic reactions in an eye of the subject, allergic reactions  
XX in the skin of the subject, acute urticaria, psoriasis, psychogenic or  
XX allergic asthma, interstitial cystitis, bowel diseases, migraines or  
XX multiple sclerosis. The invention is also useful for preventing late  
XX phase inflammatory responses induced by protein kinase activation,  
XX preferably mitogen activated protein kinase activation, where the  
XX antiallergic agent is peptide 2, peptide 2-Succ and peptide 2-Cyc. The  
XX invention provides specific direct and targeted treatment of allergies  
XX and related inflammatory conditions. The present sequence is Galphai3  
XX decapeptide  
XX Sequence 10 AA;

Query Match 100.0%; Score 57; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00099;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKECGLY 10  
|||||

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:51:16 ; Search time 19.1935 Seconds  
(without alignments)  
45.604 Million cell updates/sec

Title: US-10-009-809-1  
Perfect score: 57  
Sequence: 1 KNNLKECGLY 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents AA.\*

- 1: /EMC Celerra\_SIDS3/ptodata/2/iaa/5 COMB.pap.\*
- 2: /EMC Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pap.\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pap.\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/iaa/H COMB.pap.\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/iaa/PTUS COMB.pap.\*
- 6: /EMC Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pap.\*
- 7: /EMC Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	11	2	US-09-489-156-39
2	57	100.0	13	2	US-09-489-156-18
3	57	100.0	295	2	US-09-949-016-10678
4	57	100.0	354	2	US-09-949-016-6727
5	50	87.7	10	1	US-08-019-073-19
6	50	87.7	10	1	US-08-429-964-50
7	50	87.7	10	5	PCT-US93-08062-50
8	50	87.7	10	5	PCT-US94-01768-19
9	50	87.7	10	7	5428134-6
10	50	87.7	10	7	5436320-6
11	50	87.7	13	2	US-09-489-156-16
12	50	87.7	355	3	US-09-947-953A-10
13	50	87.7	395	2	US-09-949-016-11560
14	50	87.7	709	2	US-09-826-509-589
15	44	77.2	10	7	5428134-1
16	44	77.2	10	7	5428134-10
17	44	77.2	10	7	5436320-1
18	44	77.2	10	7	5436320-7
19	44	77.2	11	1	US-07-868-353A-7
20	44	77.2	11	1	US-08-407-804-7
21	44	77.2	11	2	US-09-124-807-7
22	44	77.2	13	2	US-09-489-156-15
23	44	77.2	40	1	US-07-868-353A-3
24	44	77.2	40	1	US-08-407-804-3
25	44	77.2	40	2	US-09-124-807-3
26	44	77.2	350	1	US-07-868-353A-14

1	US-08-407-804-23	Sequence 23, Appl
2	US-09-124-807-23	Sequence 23, Appl
3	US-07-868-353A-12	Sequence 12, Appl
4	US-07-868-353A-13	Sequence 13, Appl
5	US-07-868-353A-15	Sequence 15, Appl
6	US-08-407-804-21	Sequence 21, Appl
7	US-08-407-804-22	Sequence 22, Appl
8	US-08-407-804-24	Sequence 24, Appl
9	US-09-124-807-21	Sequence 21, Appl
10	US-09-124-807-22	Sequence 22, Appl
11	US-09-124-807-24	Sequence 24, Appl
12	US-09-984-292-7	Sequence 7, Appl
13	5428134-4	Patent No. 5428134
14	5436320-4	Patent No. 5436320
15	US-09-489-156-20	Sequence 20, Appl
16	US-09-949-016-7936	Sequence 7936, Ap
17	US-08-630-916A-48	Sequence 48, Appl
18	US-08-019-073-5	Sequence 5, Appl
19	PCT-US94-01768-5	Sequence 5, Appl
20	US-08-019-073-6	Sequence 6, Appl
21	PCT-US94-01768-6	Sequence 6, Appl
22	US-09-270-767-32429	Sequence 32429, A
23	US-09-270-767-47646	Sequence 47646, A
24	US-09-070-060-4	Sequence 4, Appl
25	US-09-357-746-4	Sequence 4, Appl
26	US-09-984-292-6	Sequence 6, Appl
27	US-09-984-292-18	Sequence 18, Appl
28	US-09-984-292-19	Sequence 19, Appl
29	US-09-984-292-12	Sequence 12, Appl
30	US-09-984-292-13	Sequence 13, Appl
31	US-09-984-292-22	Sequence 22, Appl
32	US-09-984-292-23	Sequence 23, Appl
33	US-08-630-916A-46	Sequence 46, Appl
34	US-08-446-855A-2	Sequence 2, Appl
35	US-08-150-741-2	Sequence 2, Appl
36	US-09-270-767-32417	Sequence 32417, A
37	US-09-949-016-9436	Sequence 9436, Ap
38	US-09-949-016-6891	Sequence 6891, Ap
39	US-09-949-016-9904	Sequence 9904, Ap
40	US-08-019-073-26	Sequence 26, Appl
41	PCT-US94-01768-26	Sequence 26, Appl
42	US-08-019-073-3	Sequence 3, Appl
43	US-08-019-073-20	Sequence 20, Appl
44	US-08-019-073-21	Sequence 21, Appl
45	PCT-US94-01768-3	Sequence 3, Appl
46	PCT-US94-01768-20	Sequence 20, Appl
47	PCT-US94-01768-21	Sequence 21, Appl
48	US-08-019-073-4	Sequence 4, Appl
49	PCT-US94-01768-4	Sequence 4, Appl
50	US-09-489-156-40	Sequence 40, Appl
51	US-09-489-156-19	Sequence 19, Appl
52	US-09-248-796A-16188	Sequence 16188, A
53	US-09-744-016A-27	Sequence 27, Appl
54	US-09-248-796A-19157	Sequence 19157, A
55	US-08-936-165A-461	Sequence 461, App
56	US-09-902-540-16729	Sequence 16729, A
57	US-09-270-767-57907	Sequence 57907, A
58	US-09-270-767-42597	Sequence 42597, A
59	US-09-134-001C-3586	Sequence 3586, Ap
60	US-09-248-796A-14427	Sequence 14427, A
61	US-08-019-073-2	Sequence 2, Appl
62	US-08-019-073-24	Sequence 24, Appl
63	US-08-019-073-31	Sequence 31, Appl
64	PCT-US94-01768-2	Sequence 2, Appl
65	PCT-US94-01768-31	Sequence 31, Appl
66	US-08-019-073-32	Sequence 32, Appl
67	PCT-US94-01768-32	Sequence 32, Appl
68	US-09-270-767-44014	Sequence 44014, A
69	US-09-248-796A-16913	Sequence 16913, A
70	US-09-328-352-6845	Sequence 6845, Ap
71	US-09-489-039A-10883	Sequence 10883, A
72	US-09-107-532A-4219	Sequence 4219, Ap

100 34 59.6 786 2 US-09-248-796A-15288 Sequence 15288, A

## ALIGNMENTS

RESULT 1  
US-09-489-156-39  
; Sequence 39, Application US/09489156  
; Patent No. 6559128  
; GENERAL INFORMATION:  
; APPLICANT: HAMM, Heidi  
; TITLE OF INVENTION: INHIBITORS OF G PROTEIN-MEDIATED SIGNALING, METHODS OF MAKING THE  
; FILE REFERENCE: 0290-29 (NU 99037)  
; CURRENT APPLICATION NUMBER: US/09/489,156  
; CURRENT FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 39  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-489-156-39

Query Match 100.0%; Score 57; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00047;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKECGLY 10  
Db 2 KNNLKECGLY 11

RESULT 2  
US-09-489-156-18  
; Sequence 18, Application US/09489156  
; Patent No. 6559128  
; GENERAL INFORMATION:  
; APPLICANT: HAMM, Heidi  
; TITLE OF INVENTION: INHIBITORS OF G PROTEIN-MEDIATED SIGNALING, METHODS OF MAKING THE  
; FILE REFERENCE: 0290-29 (NU 99037)  
; CURRENT APPLICATION NUMBER: US/09/489,156  
; CURRENT FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 18  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: G alpha i 3 peptide  
US-09-489-156-18

Query Match 100.0%; Score 57; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00056;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKECGLY 10  
Db 4 KNNLKECGLY 13

RESULT 3  
US-09-949-016-10678  
; Sequence 10678, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 10678  
; LENGTH: 295  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10678

Query Match 100.0%; Score 57; DB 2; Length 295;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKECGLY 10  
Db 286 KNNLKECGLY 295

RESULT 4  
US-09-949-016-6727  
; Sequence 6727, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 6727  
; LENGTH: 354  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6727

Query Match 100.0%; Score 57; DB 2; Length 354;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNLKECGLY 10  
Db 345 KNNLKECGLY 354

RESULT 5  
US-08-019-073-19  
; Sequence 19, Application US/08019073  
; Patent No. 5559209  
; GENERAL INFORMATION:  
; APPLICANT: Nishimoto, Ikuro  
; TITLE OF INVENTION: REGULATOR REGIONS OF G  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:55:10 ; Search time 37.0968 Seconds  
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Title: US-10-009-809-1  
Perfect score: 57  
Sequence: 1 KNNLKBCGLY 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications\_AA\_Main.\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	57	100.0	10	4	US-10-465-826-3
3	57	100.0	11	3	US-09-852-910-21
4	57	100.0	11	4	US-10-373-540-39
5	57	100.0	11	4	US-10-411-336A-21
6	57	100.0	13	4	US-10-373-540-18
7	57	100.0	25	4	US-10-465-826-14
8	57	100.0	26	4	US-10-465-826-9
9	57	100.0	26	4	US-10-465-826-13
10	57	100.0	26	4	US-10-465-826-15
11	57	100.0	26	4	US-10-465-826-23
12	57	100.0	26	4	US-10-465-826-24
13	57	100.0	26	4	US-10-465-826-26
14	57	100.0	26	4	US-10-465-826-29
15	57	100.0	354	3	US-09-952-680A-21
16	57	100.0	354	5	US-10-215-982-21
17	57	100.0	354	5	US-10-732-923-7596
18	57	100.0	354	5	US-10-732-923-7639
19	57	100.0	354	5	US-10-732-923-7665
20	57	100.0	354	5	US-10-732-923-7668
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23	57	100.0	354	5	US-10-732-923-7980
24	53	93.0	10	4	US-10-465-826-4
25	53	93.0	26	4	US-10-465-826-10
26	53	93.0	26	4	US-10-465-826-19
27	52	91.2	10	4	US-10-465-826-6

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29	51	89.5	10	4	US-10-465-826-5	Sequence 5, Appl
30	51	89.5	10	4	US-10-465-826-8	Sequence 8, Appl
31	51	89.5	26	4	US-10-465-826-11	Sequence 11, Appl
32	51	89.5	26	4	US-10-465-826-17	Sequence 17, Appl
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34	50	87.7	10	4	US-10-465-826-31	Sequence 31, Appl
35	50	87.7	11	3	US-09-852-910-17	Sequence 17, Appl
36	50	87.7	11	4	US-10-411-336A-17	Sequence 17, Appl
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40	50	87.7	132	5	US-10-732-923-7631	Sequence 7631, Ap
41	50	87.7	157	5	US-10-732-923-8027	Sequence 8027, Ap
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47	50	87.7	339	4	US-10-108-260A-3821	Sequence 3821, Ap
48	50	87.7	339	5	US-10-732-923-7893	Sequence 7893, Ap
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50	50	87.7	347	5	US-10-732-923-7941	Sequence 7941, Ap
51	50	87.7	349	5	US-10-732-923-7977	Sequence 7977, Ap
52	50	87.7	353	4	US-10-059-266B-18	Sequence 18, Appl
53	50	87.7	353	5	US-10-732-923-7636	Sequence 7636, Ap
54	50	87.7	353	5	US-10-732-923-7637	Sequence 7637, Ap
55	50	87.7	353	5	US-10-732-923-7638	Sequence 7638, Ap
56	50	87.7	353	5	US-10-732-923-7661	Sequence 7661, Ap
57	50	87.7	354	3	US-09-952-680A-19	Sequence 19, Appl
58	50	87.7	354	4	US-10-352-843-14	Sequence 14, Appl
59	50	87.7	354	4	US-10-059-266B-4	Sequence 4, Appl
60	50	87.7	354	5	US-10-215-982-19	Sequence 19, Appl
61	50	87.7	354	5	US-10-732-923-7635	Sequence 7635, Ap
62	50	87.7	354	5	US-10-732-923-7663	Sequence 7663, Ap
63	50	87.7	354	5	US-10-732-923-7664	Sequence 7664, Ap
64	50	87.7	354	5	US-10-732-923-7686	Sequence 7686, Ap
65	50	87.7	354	5	US-10-732-923-7879	Sequence 7879, Ap
66	50	87.7	354	5	US-10-732-923-7889	Sequence 7889, Ap
67	50	87.7	354	5	US-10-732-923-7921	Sequence 7921, Ap
68	50	87.7	354	5	US-10-732-923-7925	Sequence 7925, Ap
69	50	87.7	354	5	US-10-732-923-7933	Sequence 7933, Ap
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71	50	87.7	354	5	US-10-732-923-7948	Sequence 7948, Ap
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74	50	87.7	354	5	US-10-732-923-7976	Sequence 7976, Ap
75	50	87.7	354	5	US-10-732-923-8043	Sequence 8043, Ap
76	50	87.7	354	5	US-09-947-953-2	Sequence 2, Appl
77	50	87.7	355	3	US-09-952-680A-20	Sequence 20, Appl
78	50	87.7	355	3	US-09-952-680A-23	Sequence 23, Appl
79	50	87.7	355	3	US-10-116-275-267	Sequence 267, App
80	50	87.7	355	4	US-10-408-765A-427	Sequence 427, App
81	50	87.7	355	4	US-10-408-765A-2332	Sequence 2332, Ap
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83	50	87.7	355	5	US-10-215-982-23	Sequence 23, Appl
84	50	87.7	355	5	US-10-855-892-10	Sequence 10, Appl
85	50	87.7	355	5	US-10-855-899-10	Sequence 10, Appl
86	50	87.7	355	5	US-10-855-805-10	Sequence 10, Appl
87	50	87.7	355	5	US-10-732-923-7598	Sequence 7598, Ap
88	50	87.7	355	5	US-10-732-923-7599	Sequence 7599, Ap
89	50	87.7	355	5	US-10-732-923-7642	Sequence 7642, Ap
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91	50	87.7	355	5	US-10-732-923-7667	Sequence 7667, Ap
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94	50	87.7	355	5	US-10-732-923-7943	Sequence 7943, Ap
95	50	87.7	355	5	US-10-732-923-7971	Sequence 7971, Ap
96	50	87.7	355	5	US-10-732-923-7982	Sequence 7982, Ap
97	50	87.7	355	5	US-10-732-923-7984	Sequence 7984, Ap
98	50	87.7	355	5	US-10-732-923-7985	Sequence 7985, Ap
99	50	87.7	355	5	US-10-732-923-7986	Sequence 7986, Ap
100	50	87.7	355	5	US-10-732-923-8035	Sequence 8035, Ap

## ALIGNMENTS

RESULT 1  
US-10-465-826-1  
; Sequence 1, Application US/10465826  
; Publication No. US20040137006A1  
; GENERAL INFORMATION:  
; APPLICANT: ALLERGENE LTD.  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: ALL/002 US  
; CURRENT APPLICATION NUMBER: US/10/465,826  
; CURRENT FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Decapeptide derived from Homo sapiens G-alpha-i3  
US-10-465-826-1  
  
Query Match 100.0%; Score 57; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 KNNLKECGLY 10  
  
RESULT 2  
US-10-465-826-3  
; Sequence 3, Application US/10465826  
; Publication No. US20040137006A1  
; GENERAL INFORMATION:  
; APPLICANT: ALLERGENE LTD.  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: ALL/002 US  
; CURRENT APPLICATION NUMBER: US/10/465,826  
; CURRENT FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; NAME/KEY: BINDING  
; LOCATION: (1)..(10)  
; OTHER INFORMATION: A bond exists between the side chain of K at position 1 and the  
; OTHER INFORMATION: -terminus of the peptide  
US-10-465-826-3  
  
Query Match 100.0%; Score 57; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KNNLKECGLY 10  
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DB 1 KNNLKECGLY 10  
  
RESULT 3  
US-09-852-910-21  
; Sequence 21, Application US/09852910  
; Publication No. US20030096297A1  
; GENERAL INFORMATION:  
; APPLICANT: Hamm, Heidi  
; APPLICANT: Gilchrist, Annette  
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor S;  
; FILE REFERENCE: 2661-101  
; CURRENT APPLICATION NUMBER: US/09/852,910  
; CURRENT FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US 60/275,472  
; PRIOR FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 271  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 21  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 2 KNNLKECGLY 11  
  
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US-10-373-540-39  
; Sequence 39, Application US/10373540  
; Publication No. US20030162258A1  
; GENERAL INFORMATION:  
; APPLICANT: HAMM, Heidi  
; APPLICANT: GILCHRIST, Annette  
; TITLE OF INVENTION: INHIBITORS OF G PROTEIN-MEDIATED SIGNALING, METHODS OF MAKING THEM  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 0290-29 (NU 99037)  
; CURRENT APPLICATION NUMBER: US/10/373,540  
; CURRENT FILING DATE: 2003-02-24  
; PRIOR APPLICATION NUMBER: US/09/489,156  
; PRIOR FILING DATE: PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 47  
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
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Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 2 KNNLKECGLY 11  
  
RESULT 5  
US-10-411-336A-21  
; Sequence 21, Application US/10411336A  
; Publication No. US20040018558A1  
; GENERAL INFORMATION:  
; APPLICANT: GILCHRIST, ANNETTE  
; APPLICANT: HAMM, HEIDI  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR  
; TITLE OF INVENTION: SIGNALING



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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:55:23 ; Search time 2.74194 Seconds  
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Title: US-10-009-809-1  
Perfect score: 57  
Sequence: 1 KNNLKEGGLY 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 100 summaries

Database : Published Applications AA New:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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12	53	93.0	26	7	US-11-214-588-10
13	53	93.0	26	7	US-11-214-588-19
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15	52	91.2	26	7	US-11-214-588-16
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19	51	89.5	26	7	US-11-214-588-17
20	51	89.5	26	7	US-11-214-588-20
21	50	87.7	10	7	US-11-214-588-31
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23	50	87.7	339	7	US-11-293-697-3821
24	49	86.0	26	7	US-11-214-588-18
25	47	82.5	10	7	US-11-214-588-7

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27	47	82.5	26	7	US-11-214-588-12	Sequence 12, Appl
28	47	82.5	26	7	US-11-214-588-21	Sequence 21, Appl
29	47	82.5	26	7	US-11-214-588-30	Sequence 30, Appl
30	44	77.2	10	7	US-11-214-588-2	Sequence 2, Appl
31	44	77.2	26	7	US-11-214-588-25	Sequence 25, Appl
32	37	64.9	894	6	US-10-449-902-43384	Sequence 43384, A
33	37	64.9	955	6	US-10-449-902-54693	Sequence 54693, A
34	37	63.2	266	6	US-10-471-571A-708	Sequence 708, App
35	36	63.2	266	6	US-10-471-571A-29471	Sequence 29471, A
36	36	63.2	266	6	US-10-471-571A-29470	Sequence 29470, A
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49	33	57.9	228	6	US-10-471-571A-5434	Sequence 5434, Ap
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51	33	57.9	342	6	US-10-449-902-20188	Sequence 20188, A
52	33	57.9	364	6	US-10-449-902-36200	Sequence 36200, A
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62	33	57.9	581	6	US-10-449-902-54588	Sequence 54588, A
63	33	57.9	586	6	US-10-449-902-54588	Sequence 54588, A
64	33	57.9	590	6	US-10-449-902-54588	Sequence 54588, A
65	33	57.9	639	7	US-11-293-697-3966	Sequence 3966, Ap
66	33	57.9	674	7	US-11-251-208-31	Sequence 31, Appl
67	33	57.9	1367	7	US-11-289-102-382	Sequence 382, App
68	32	56.1	50	6	US-10-449-902-29657	Sequence 29657, A
69	32	56.1	53	6	US-10-449-902-29656	Sequence 29656, A
70	32	56.1	395	6	US-10-449-902-3382	Sequence 3382, Ap
71	32	56.1	427	6	US-10-449-902-49898	Sequence 49898, A
72	32	56.1	546	6	US-10-449-902-41589	Sequence 41589, A
73	32	56.1	620	6	US-10-449-902-54390	Sequence 54390, A
74	32	56.1	673	6	US-10-449-902-53706	Sequence 53706, A
75	31	54.4	23	7	US-11-134-871-1286	Sequence 1286, Ap
76	31	54.4	75	6	US-10-449-902-18313	Sequence 18313, A
77	31	54.4	213	7	US-11-174-307B-4516	Sequence 4516, Ap
78	31	54.4	214	6	US-10-449-902-49637	Sequence 49637, A
79	31	54.4	217	6	US-10-449-902-37834	Sequence 37834, A
80	31	54.4	220	6	US-10-449-902-49637	Sequence 49637, A
81	31	54.4	224	6	US-10-449-902-54551	Sequence 54551, A
82	31	54.4	225	6	US-10-449-902-54551	Sequence 54551, A
83	31	54.4	227	6	US-10-449-902-54551	Sequence 54551, A
84	31	54.4	229	6	US-10-449-902-54551	Sequence 54551, A
85	31	54.4	251	6	US-10-449-902-55435	Sequence 55435, A
86	31	54.4	251	6	US-10-449-902-55435	Sequence 55435, A
87	31	54.4	286	6	US-10-449-902-17202	Sequence 17202, A
88	31	54.4	306	6	US-10-449-902-3526	Sequence 3526, Ap
89	31	54.4	351	6	US-10-449-902-3526	Sequence 3526, Ap
90	31	54.4	352	6	US-10-449-902-3526	Sequence 3526, Ap
91	31	54.4	355	6	US-10-449-902-3526	Sequence 3526, Ap
92	31	54.4	358	6	US-10-449-902-3526	Sequence 3526, Ap
93	31	54.4	363	6	US-10-449-902-3526	Sequence 3526, Ap
94	31	54.4	366	6	US-10-449-902-3526	Sequence 3526, Ap
95	31	54.4	387	6	US-10-449-902-3526	Sequence 3526, Ap
96	31	54.4	389	6	US-10-449-902-3526	Sequence 3526, Ap
97	31	54.4	392	6	US-10-449-902-3526	Sequence 3526, Ap
98	31	54.4	416	6	US-10-449-902-3526	Sequence 3526, Ap

99 31 54.4 433 6 US-10-449-902-51082 Sequence 51082, A  
100 31 54.4 452 6 US-10-449-902-53954 Sequence 53954, A

## ALIGNMENTS

RESULT 1  
US-11-214-588-1  
; Sequence 1, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Decapeptide derived from Homo sapiens G-alpha-i3  
US-11-214-588-1

Query Match 100.0%; Score 57; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKECGLY 10  
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Db 1 KNNLKECGLY 10

RESULT 2  
US-11-214-588-3  
; Sequence 3, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (1)...(10)  
; OTHER INFORMATION: A bond exists between the side chain of K at position 1 and the  
; OTHER INFORMATION: c-terminus of the peptide  
US-11-214-588-3

Query Match 100.0%; Score 57; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0001;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNNLKECGLY 10  
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Db 1 KNNLKECGLY 10

RESULT 3  
US-11-214-588-14  
; Sequence 14, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 14  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-214-588-14

Query Match 100.0%; Score 57; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.00025;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKECGLY 10  
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Db 16 KNNLKECGLY 25

RESULT 4  
US-11-214-588-9  
; Sequence 9, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 9  
; LENGTH: 26  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-214-588-9

Query Match 100.0%; Score 57; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKECGLY 10  
| | | | | | | | | |  
Db 17 KNNLKECGLY 26

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:50:59 ; Search time 4.83871 Seconds  
(without alignments)  
198.848 Million cell updates

Title: US-10-009-809-1  
Perfect score: 57  
Sequence: 1 KNNLKECGLY 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 10%

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Database :      PIR_80:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	57	100.0	63	2	I48071	GRP-binding protei	
2	57	100.0	354	1	RGHUI3	GRP-binding regula	
3	57	100.0	354	1	RGHUI3	GRP-binding regula	
4	57	100.0	354	2	S28157	GRP-binding regula	
5	57	100.0	354	2	S40508	GRP-binding regula	
6	57	100.0	354	2	S40509	G-protein - chicke	
7	50	87.7	354	1	RGBOI1	GRP-binding regula	
8	50	87.7	354	1	RGHUI1	GRP-binding regula	
9	50	87.7	354	1	RGHUI1	GRP-binding regula	
10	50	87.7	354	1	RGXLI1	GRP-binding regula	
11	50	87.7	354	2	S28157	GRP-binding regula	
12	50	87.7	354	2	S24362	GRP-binding regula	
13	50	87.7	354	2	I50237	GRP-binding regula	
14	50	87.7	354	2	S27013	GRP-binding regula	
15	50	87.7	355	1	RGHUI2	GRP-binding regula	
16	50	87.7	355	1	RGMSI2	GRP-binding regula	
17	50	87.7	355	1	RGMTI2	GRP-binding regula	
18	50	87.7	355	2	S28158	GRP-binding regula	
19	50	87.7	355	2	I50238	G12 protein alpha	
20	50	87.7	355	2	A61031	GRP-binding regula	
21	50	87.7	355	2	A48976	GRP-binding regula	
22	46	80.7	345	1	RGXLI3	GRP-binding regula	
23	45	78.9	104	2	B35888	probable GTP-bindi	
24	44	77.2	350	1	RGBOT1	GRP-binding regula	
25	44	77.2	350	1	RGHUT1	GRP-binding regula	
26	44	77.2	350	1	RGMST1	GRP-binding regula	
27	44	77.2	354	1	RGHUT2	GRP-binding regula	
28	44	77.2	354	1	RGHUT2	GRP-binding regula	
29	44	77.2	354	2	S24352	gustducin - rat	

## ALIGNMENTS

## RESULT 1

I48071  
 GTP binding protein - Chinese hamster (fragment)  
 C:Species: Cricetus griseus (Chinese hamster)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I48071  
 R:Baron, B.; Fernandez, M.A.; Toledo, F.; Le Roscouet, D.; Mayau, V.; Martin, N.; Buttin  
 Genomics 24, 288-294, 1994  
 A>Title: The highly conserved Chinese hamster GNAI3 gene maps less than 60 kb from the A  
 A:Reference number: I48071; MUID:95213019; PMID:7698751  
 A:Accession: I48071  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-63 <RES>  
 A:CROSS-references: UNIPROT:Q60397; UNIPARC:UPI000012B200; EMBL:X79282; NID:g642170; PID  
 C:Genetics:  
 A:Gene: Galphai3  
 C:Superfamily: GTP-binding regulatory protein Gs alpha chain

Query Match 100.0%; Score 57; DB 2; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0.0019;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KNNLKECGLY 10  
 |||||  
 Db 54 KNNLKECGLY 63  
 RESULT 2  
 RGHU13  
 N;Alternate names: GTP-binding regulatory protein Gi alpha-3 chain (adenylate cyclase-inhibiting) - human  
 C:Species: Homo sapiens (man)  
 C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C:Accession: S02348; S00055; A32139; C28154; A28157; S00078  
 R:Beale, C.R.; Wilson, C.B.; Ferlmutter, R.M.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 7886-7890, 1987  
 A>Title: A small multigene family encodes G(i) signal-transduction proteins.  
 A:Reference number: S02319; MUID:88068503; PMID:3120178  
 A:Accession: S02348  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <BEA>  
 A:CROSS-references: UNIPROT:P08754; UNIPARC:UPI000004D205; EMBL:J03005; NID:g183183; PID  
 R:DiDebury, J.R.; Snyderman, R.  
 FEBS Lett. 219, 259-263, 1987  
 A>Title: Molecular cloning of a new human G protein. Evidence for two G(i-alpha)-like pr  
 A:Reference number: S00055; MUID:87247315; PMID:3109953  
 A:Accession: S00055  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <DID>  
 A:CROSS-references: UNIPARC:UPI000004D205; EMBL:M27543; NID:g183395; PIDN:AAA52579.1; PI  
 A>Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in having 17-Met  
 R:Kim, S.; Ang, S.L.; Bloch, D.B.; Bloch, K.D.; Kawahara, Y.; Tolman, C.; Lee, R.; Seidm  
 Proc. Natl. Acad. Sci. U.S.A. 85, 4153-4157, 1988  
 A>Title: Identification of cDNA encoding an additional alpha-subunit of a human GTP-bind  
 A:Reference number: A32139; MUID:88247980; PMID:3132707  
 A:Accession: A32139  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <KIM>  
 A:CROSS-references: UNIPARC:UPI000004D205; GB:J03238; NID:g183686; PIDN:AAA55939.1; PID:  
 R:Itoh, H.; Toyama, R.; Kozasa, T.; Tsukamoto, T.; Matsuoka, M.; Kaziro, Y.  
 J. Biol. Chem. 263, 6656-6664, 1988  
 A>Title: Presence of three distinct molecular species of G-i protein alpha-subunit. Stru  
 A:Reference number: A28154; MUID:88198230; PMID:2834384  
 A:Accession: C28154  
 A:Molecule type: DNA  
 A:Residues: 1-354 <ITO>  
 A:CROSS-references: UNIPARC:UPI000004D205; GB:J03220  
 R:Codina, J.; Olate, J.; Abramowitz, J.; Mattera, R.; Cook, R.G.; Birnbaumer, L.  
 J. Biol. Chem. 263, 6746-6750, 1988

A>Title: Alpha-i-3 cDNA encodes the alpha-subunit of G-K, the stimulatory G protein of re  
 A:Reference number: A28157; MUID:88198244; PMID:2452165  
 A:Accession: A28157  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <COD>  
 A:CROSS-references: UNIPARC:UPI000004D205; GB:J03198; NID:g183224; PIDN:AAA35896.1; PID:  
 R:Suki, W.N.; Abramowitz, J.; Mattera, R.; Codina, J.; Birnbaumer, L.  
 FEBS Lett. 220, 187-192, 1987  
 A>Title: The human genome encodes at least three non-allelic G proteins with alpha(i)-5  
 A:Reference number: S00078; MUID:87276552; PMID:2440724  
 A:Accession: S00078  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <SUK>  
 A:CROSS-references: UNIPARC:UPI00001740E9  
 C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay  
 ains. The beta and gamma chains, required for GTPase activity, appear to be common to all  
 rase; it is specific for each type of G protein.  
 C:Comment: The Gi alpha chain is specific for G protein that is involved in hormonal regu  
 C:Genetics:  
 A:Gene: GDB:GNAI3  
 A:CROSS-references: GDB:119276; OMIM:119370  
 A:Map position: 1p13-1p13  
 C:Superfamily: GTP-binding regulatory protein Gs alpha chain  
 C:Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; nuc  
 F;2-354/Product: GTP-binding regulatory protein Gi alpha-3 chain #status predicted <MAR>  
 F;40-47/Region: nucleotide-binding motif A (P-loop)  
 F;269-272/Region: GTP-binding NKXD motif  
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F;3/Binding site: palmitate (Cys) (covalent) #status predicted  
 F;178/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted  
 F;351/Modified site: ADP-ribosylcysteine (Cys) (by pertussis toxin) #status predicted  
 Query Match 100.0%; Score 57; DB 1; Length 354;  
 Best Local Similarity 100.0%; Pred. No. 0.0094;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KNNLKECGLY 10  
 |||||  
 Db 345 KNNLKECGLY 354  
 RESULT 3  
 RGP13  
 GTP-binding regulatory protein Gi alpha-3 chain (adenylate cyclase-inhibiting) - rat  
 N;Alternate names: GTP-binding regulatory protein Gk alpha chain; guanine nucleotide bin  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004  
 C:Accession: E27423; A28154; C35377  
 R:Jones, D.T.; Reed, R.R.  
 J. Biol. Chem. 262, 14241-14249, 1987  
 A>Title: Molecular cloning of five GTP-binding protein cDNA species from rat olfactory ne  
 A:Reference number: A92614; MUID:88007678; PMID:2820999  
 A:Accession: E27423  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <JON>  
 A:CROSS-references: UNIPROT:P08753; UNIPARC:UPI0000167949; GB:M20713; NID:g203163; PIDN:  
 R:Itoh, H.; Toyama, R.; Kozasa, T.; Tsukamoto, T.; Matsuoka, M.; Kaziro, Y.  
 J. Biol. Chem. 263, 6656-6664, 1988  
 A>Title: Presence of three distinct molecular species of G-i protein alpha-subunit. Stru  
 A:Reference number: A28154; MUID:88198230; PMID:2834384  
 A:Accession: A28154  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <ITO>  
 A:CROSS-references: UNIPARC:UPI0000167949; GB:J03219; NID:g204320; PIDN:AAA41224.1; PID:  
 R:Linder, M.E.; Ewald, D.A.; Miller, R.J.; Gilman, A.G.  
 J. Biol. Chem. 265, 8243-8251, 1990  
 A>Title: Purification and characterization of G-alpha and three types of G-ialpha after  
 A:Reference number: A35377; MUID:90243707; PMID:2159473  
 A:Accession: C35377  
 A>Status: preliminary  
 A:Molecule type: protein

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:50:27 ; Search time 36.9355 Seconds  
(without alignments)  
250.441 Million cell updates/sec

Title: US-10-009-809-1

Perfect score: 57

Sequence: 1 KNNLKECGLY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt\_7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	63	1	GNAI3_CRIGR
2	57	100.0	89	2	Q8QGZ2_FUGRU
3	57	100.0	346	2	Q45QM8_RAT
4	57	100.0	353	1	GNAI3_CAVPO
5	57	100.0	353	1	GNAI3_HUMAN
6	57	100.0	353	1	GNAI3_MOUSE
7	57	100.0	353	1	GNAI3_RAT
8	57	100.0	354	2	Q5TZX1_HUMAN
9	57	100.0	354	2	Q3ZCA7_BOVIN
10	57	100.0	354	2	Q3HR12_CRIGR
11	57	100.0	354	2	Q3TGV1_MOUSE
12	57	100.0	354	2	Q3TUH1_MOUSE
13	57	100.0	354	2	Q90846_CHICK
14	57	100.0	354	2	Q90847_CHICK
15	50	87.7	53	2	Q922V6_MOUSE
16	50	87.7	132	2	Q8JZT4_MOUSE
17	50	87.7	137	2	Q6LCB5_HUMAN
18	50	87.7	301	2	Q9Y206_HYDWA
19	50	87.7	347	2	Q7ZW15_BRARE
20	50	87.7	353	1	GNAI1_BOVIN
21	50	87.7	353	1	GNAI1_CAVPO
22	50	87.7	353	1	GNAI1_CHICK
23	50	87.7	353	1	GNAI1_HUMAN
24	50	87.7	353	1	GNAI1_ORYLA
25	50	87.7	353	1	GNAI1_PONPY
26	50	87.7	353	1	GNAI1_RAT
27	50	87.7	353	1	GNAI1_XENLA
28	50	87.7	353	1	GNAI_4STPE
29	50	87.7	353	1	GNAI_HELTI
30	50	87.7	353	1	GNAI_LYNST
31	50	87.7	353	2	Q5DBN1_SCHJA

32	50	87.7	353	2	Q7Q6E0_ANOGA
33	50	87.7	353	2	Q5R9N4_PONPY
34	50	87.7	354	1	GNAI2_CANFA
35	50	87.7	354	1	GNAI2_CAVPO
36	50	87.7	354	1	GNAI2_CHICK
37	50	87.7	354	1	GNAI2_HUMAN
38	50	87.7	354	1	GNAI2_WACFA
39	50	87.7	354	1	GNAI2_MOUSE
40	50	87.7	354	1	GNAI2_ORYLA
41	50	87.7	354	1	GNAI2_RAT
42	50	87.7	354	1	GNAI_HOMAM
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44	50	87.7	354	2	Q6QM17_STRPU
45	50	87.7	354	2	Q8WP45_HALRO
46	50	87.7	354	2	Q8WSS1_CIOIN
47	50	87.7	354	2	Q8WSS2_CIOIN
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53	50	87.7	354	2	Q6GPC5_XENLA
54	50	87.7	354	2	Q7T3D3_BRARE
55	50	87.7	355	2	Q96C71_HUMAN
56	50	87.7	355	2	Q3HR13_CRIGR
57	50	87.7	355	2	Q3TXK7_MOUSE
58	50	87.7	355	2	Q45QN0_RAT
59	50	87.7	355	2	Q5U4X0_XENLA
60	50	87.7	355	2	Q6P3M7_XENTR
61	50	87.7	355	2	Q6TNT8_BRARE
62	50	87.7	355	2	Q9W6A4_SQUAC
63	50	87.7	377	2	Q7ZW82_BRARE
64	50	87.7	404	2	Q4SAC0_TETNG
65	50	87.7	499	2	Q4RXT7_TETNG
66	47	82.5	82	2	Q8QGY6_FUGRU
67	46	80.7	345	1	GNAI3_XENLA
68	46	80.7	354	2	Q5I080_XENTR
69	46	80.7	354	2	Q7ZXT7_XENLA
70	45	78.9	328	2	Q8IT62_SCHMA
71	44	77.2	47	2	Q8QGY9_FUGRU
72	44	77.2	157	2	Q8BSY7_MOUSE
73	44	77.2	222	2	Q4TH72_TETNG
74	44	77.2	336	2	Q4RV86_TETNG
75	44	77.2	343	2	Q9D7B3_MOUSE
76	44	77.2	349	1	GNAI1_BOVIN
77	44	77.2	349	1	GNAI1_CANFA
78	44	77.2	349	1	GNAI1_HUMAN
79	44	77.2	349	1	GNAI1_MOUSE
80	44	77.2	349	1	GNAI1_XENLA
81	44	77.2	350	2	Q4VBN2_HUMAN
82	44	77.2	350	2	P79895_SPAU
83	44	77.2	350	2	Q2T914_XENLA
84	44	77.2	350	2	Q4L222_GEGCE
85	44	77.2	350	2	Q4RAX7_TETNG
86	44	77.2	350	2	Q6DJF0_XENLA
87	44	77.2	350	2	Q90WX6_BRARE
88	44	77.2	350	2	Q9DG28_CHICK
89	44	77.2	350	2	Q9YI23_AMBTI
90	44	77.2	353	1	GNAI2_BOVIN
91	44	77.2	353	1	GNAI2_HUMAN
92	44	77.2	353	1	GNAI2_MOUSE
93	44	77.2	353	1	GNAI3_RAT
94	44	77.2	354	2	Q5T697_HUMAN
95	44	77.2	354	2	Q90WX5_BRARE
96	44	77.2	354	2	Q9DG27_CHICK
97	44	77.2	358	2	Q8QGY3_FUGRU
98	44	77.2	371	2	Q8QGY8_FUGRU
99	43	75.4	426	2	Q4RXB3_TETNG
100	43	75.4	1121	2	Q2THX3_9VIRU

ALIGNMENTS

```

RESULT 1
GNAI3_CRIGR
ID GNAI3_CRIGR STANDARD; PRT; 63 AA.
AC Q60397;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DE Guanine nucleotide-binding protein G(k), alpha subunit (G(i) alpha-3)
DE (Fragment).
GN Name=GNAI3;
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetidae; Cricetinae; Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=95213019; PubMed=7698751;
RA Barton B., Fernandez M.A., Toledo F., le Roscouet D., Mayau V.,
RA Martin N., Buttin G., Debatisse M.;
RT "The highly conserved Chinese hamster GNAI3 gene maps less than 60 kb
RT from the AMPD2 gene and lacks the intronic U6 snRNA present in its
RT human counterpart.";
RL Genomics 24:288-294(1994).
CC -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC involved as modulators or transducers in various transmembrane
CC signaling systems. G(k) is the stimulatory G protein of receptor-
CC regulated K(+) channels.
CC -!- SUBUNIT: G proteins are composed of 3 units: alpha, beta and
CC gamma. The alpha chain contains the guanine nucleotide binding
CC site.
CC -!- SIMILARITY: Belongs to the G-alpha family. G(i/o/t/z) subfamily.
CC
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CC
EMBL; X79282; CAAS5869.1; -; Genomic_DNA.
PIR; I48071; I48071.
HSSP; P04898; 1KJY.
SMR; Q60397; 1-63.
InterPro; IPR001019; Gprotein_alpha_bd.
InterPro; IPR001408; Gprotein_alpha_1.
Pfam; PF00503; G-alpha; 1.
PRINTS; PR00441; GPROTEINAI.
KW ADP-ribosylation; GTP-binding; Nucleotide-binding; Transducer.
CHAIN <1 63
FT Guanine nucleotide-binding protein G(k),
FT alpha subunit.
FT /FTID=PRO_0000203691.
FT MOD_RES 60 60 ADP-ribosylcysteine (by pertussis toxin)
FT (By similarity).
FT NON_TER 1 1
SQ SEQUENCE 63 AA; 7288 MW; 32C3A203F194ADB9 CRC64;

Query Match 100.0%; Score 57; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKECGLY 10
Db 54 KNNLKECGLY 63

RESULT 2
Q8QG22_FUGRU
ID Q8QG22_FUGRU PRELIMINARY; PRT; 89 AA.
AC Q8QG22;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DE Guanine nucleotide-binding protein (Fragment).
DE Guanine nucleotide-binding protein (Fragment).
GN Name=Gnai3;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97129408; PubMed=8973916;
RA Sarwal M.M., Sontag J.M., Hoang L., Brenner S., Wilkie T.M.;
RT "G protein alpha subunit multigene family in the Japanese puffer fish
RT Fugu rubripes: PCR from a compact vertebrate genome.";
RL Genome Res. 6:1207-1215(1996).
CC
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CC
EMBL; L79894; AAL77636.1; -; Genomic_DNA.
HSSP; P10824; 1GG2.
SMR; Q8QG22; 1-89.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR001019; Gprotein_alpha_bd.
DR InterPro; IPR001408; Gprotein_alpha_1.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00441; GPROTEINAI.
FT NON_TER 1
SQ SEQUENCE 89 AA; 10460 MW; D4D8749A1D2B74F7 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKECGLY 10
Db 80 KNNLKECGLY 89

RESULT 3
Q4SQM8_RAT
ID Q4SQM8_RAT PRELIMINARY; PRT; 346 AA.
AC Q4SQM8;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Guanine nucleotide binding protein alpha inhibiting 3 (Fragment).
GN Name=Gnai3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WKY, and SHR;
RA Jackson E.K., Zhu C.;
RT "Genetic Similarity Between Spontaneously Hypertensive Rats and
RT Wistar-Kyoto Rats in the Coding Regions of Signal Transduction
RT Proteins.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
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CC
EMBL; DQ120474; AA223813.1; -; mRNA.
EMBL; DQ120473; AA223812.1; -; mRNA.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001019; Gprotein_alpha_bd.
DR InterPro; IPR001408; Gprotein_alpha_1.
DR InterPro; IPR011025; GproteinA_insert.

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	57	100.0	10	2	AAR61259	Control p
2	57	100.0	10	2	AAR49785	Farnesylt
3	57	100.0	10	2	AAW04476	Weak inh1
4	57	100.0	10	5	AAR26151	Galphai2
5	57	100.0	11	6	ABJ36692	G protein
6	57	100.0	11	8	ADT51091	G protein
7	57	100.0	13	6	ABJ36771	G protein
8	57	100.0	13	7	ABW00010	Human G a
9	57	100.0	13	7	ADF45264	G alpha c
10	57	100.0	13	8	ADT51186	G protein
11	57	100.0	23	4	AAO08372	Human pol
12	57	100.0	26	4	AAI72144	Modified
13	57	100.0	27	4	AAI72145	Anti-alle
14	57	100.0	288	6	ABR41313	Human DIT
15	57	100.0	339	7	ADM051136	Human pro
16	57	100.0	339	7	ADM04957	Human pro
17	57	100.0	339	9	AEC87887	Human GDN
18	57	100.0	339	9	AEC88066	Human CDN
19	57	100.0	353	7	ADT57521	Human Pro
20	57	100.0	353	7	ADT57515	Rat Prote
21	57	100.0	353	7	ADT57517	Human Pro
22	57	100.0	353	7	ADT57519	Rat Prote
23	57	100.0	353	8	ADN06152	Rat Gli-H

97 51 89.5 353 5 ABG68602 Human G p  
 98 51 89.5 353 7 ADC12758 Adc12758 Human GPC  
 99 51 89.5 354 2 AAR42424 Aar42424 Rat Gustd  
 100 51 89.5 354 2 AAR42425 Aar42425 Bovine co

## ALIGNMENTS

## RESULT 1

AAR61259  
 ID AAR61259 standard; peptide; 10 AA.

XX AAR61259;  
 DT 25-MAR-2003 (revised)  
 DT 13-APR-1995 (first entry)  
 XX Control peptide corresponding to Gi2 alpha Lys346-Phe355.  
 DE Anticouplone; G-protein; Regulator region; Immunosuppressant.  
 KW Synthetic.  
 OS WO9419002-A1.  
 XX 01-SEP-1994.  
 XX 17-FEB-1994; 94WO-US001768.  
 XX 18-FEB-1993; 93US-00019073.  
 XX (GEHO ) GEN HOSPITAL CORP.  
 XX Nishimoto I;  
 XX WPI; 1994-293996/36.

XX Anticouplone sequences of G proteins - inhibit activation of G protein by  
 PT G-coupled receptor, used to treat neuromuscular and autoimmune diseases,  
 PT cancer, diabetes, hypertension, AIDS etc.  
 XX Disclosure; Page 8; 52pp; English.  
 XX Control peptide, showed no effect on peptide (AAR61267) induced Gi2  
 CC activation. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 10 AA;  
 Query Match 100.0%; Score 57; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10  
 |||||  
 DB 1 KNNLKDCGLF 10

## RESULT 2

AAR49785  
 ID AAR49785 standard; peptide; 10 AA.

XX AAR49785;  
 DT 25-MAR-2003 (revised)  
 DT 08-AUG-1994 (first entry)  
 XX Farnesyltransferase-inhibitor.  
 DE Farnesyltransferase-inhibitor.  
 XX Farnesyltransferase-inhibitor; farnesyltransferase; FT; p21ras;  
 KW ras protein; farnesylation; cancer therapy.  
 XX Synthetic.

XX WO9404561-A1.  
 PN 03-MAR-1994.  
 PD 24-AUG-1993; 93WO-US008062.  
 XX 24-AUG-1992; 92US-00935087.  
 PR (TEXA ) UNIV TEXAS SYSTEM.  
 PA (GETH ) GENENTECH INC.  
 XX Brown MS, Goldstein JL, Reiss Y, Marsters JC;  
 PI WPI; 1994-083105/10.  
 XX New farnesyl-transferase inhibitors - used for inhibiting attachment of a  
 PT farnesyl moiety to a p21ras protein in malignant cells.  
 XX Disclosure; Page 49; 183pp; English.  
 CC Peptides given in AAR49741-75, AAR49777-78 and AAR49785-88, which include  
 CC a family of tetrapeptides based on the recognition site (AAR49776) of  
 CC farnesyltransferase (FT), are potential anticancer agents that inhibit  
 CC FT, thereby preventing expression of p21ras. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX Sequence 10 AA;

Query Match 100.0%; Score 57; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10  
 |||||  
 DB 1 KNNLKDCGLF 10

## RESULT 3

AAW04476  
 ID AAW04476 standard; peptide; 10 AA.

XX AAW04476;  
 XX 05-AUG-1997 (first entry)  
 DT Weak inhibitor of farnesyl transferase.  
 XX Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;  
 KW ras protein; K-ras B; malignant; detection; identification.  
 XX Synthetic.  
 XX WO9634113-A2.  
 PN 31-OCT-1996.  
 PD 29-APR-1996; 96WO-US005969.  
 XX 27-APR-1995; 95US-00429964.  
 XX (TEXA ) UNIV TEXAS SYSTEM.

XX Brown MS; Goldstein JL, James GL;  
 PI WPI; 1996-497642/49.  
 XX Assay for farnesyl transferase activity - by determining ability to  
 PT transfer farnesyl moiety to K-ras B protein, partic. useful for  
 PT identifying inhibitors.  
 XX Disclosure; Page 179; 257pp; English.

QY 1 KNNLKDCGLF 10  
 |||||  
 DB 1 KNNLKDCGLF 10



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:51:16 ; Search time 19.1935 Seconds  
(without alignments)  
45.604 Million cell updates/sec

Title: US-10-009-809-2  
Perfect score: 57  
Sequence: 1 KNNLKDGLF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents\_AA\*

1: /EMC Cellerai\_SIDS3/ptodata/2/iaa/5 COMB.pap.\*  
2: /EMC Cellerai\_SIDS3/ptodata/2/iaa/6 COMB.pap.\*  
3: /EMC Cellerai\_SIDS3/ptodata/2/iaa/7 COMB.pap.\*  
4: /EMC Cellerai\_SIDS3/ptodata/2/iaa/H COMB.pap.\*  
5: /EMC Cellerai\_SIDS3/ptodata/2/iaa/PCTUS COMB.pap.\*  
6: /EMC Cellerai\_SIDS3/ptodata/2/iaa/RE COMB.pap.\*  
7: /EMC Cellerai\_SIDS3/ptodata/2/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	1	US-08-019-073-19
2	57	100.0	10	1	US-08-429-964-50
3	57	100.0	10	5	PCT-US93-08062-50
4	57	100.0	10	5	PCT-US94-01768-19
5	57	100.0	10	7	5428134-6
6	57	100.0	10	7	5436320-6
7	57	100.0	13	2	US-09-489-156-16
8	57	100.0	355	3	US-09-947-953A-10
9	57	100.0	395	2	US-09-949-016-11560
10	57	100.0	709	2	US-09-836-509-589
11	51	89.5	10	7	5428134-1
12	51	89.5	10	7	5428134-10
13	51	89.5	10	7	5436320-1
14	51	89.5	10	7	5436320-7
15	51	89.5	11	1	US-07-868-353A-7
16	51	89.5	11	1	US-08-407-804-7
17	51	89.5	11	2	US-09-124-807-7
18	51	89.5	13	2	US-09-489-156-15
19	51	89.5	40	1	US-07-868-353A-3
20	51	89.5	40	1	US-08-407-804-3
21	51	89.5	40	2	US-09-124-807-3
22	51	89.5	350	1	US-07-868-353A-14
23	51	89.5	350	1	US-08-407-804-23
24	51	89.5	350	2	US-09-124-807-23
25	51	89.5	354	1	US-07-868-353A-12
26	51	89.5	354	1	US-07-868-353A-13

27	51	89.5	354	1	US-07-868-353A-15	Sequence 15, Appl
28	51	89.5	354	1	US-08-407-804-21	Sequence 21, Appl
29	51	89.5	354	1	US-08-407-804-22	Sequence 22, Appl
30	51	89.5	354	1	US-08-407-804-24	Sequence 24, Appl
31	51	89.5	354	2	US-09-124-807-21	Sequence 21, Appl
32	51	89.5	354	2	US-09-124-807-22	Sequence 22, Appl
33	51	89.5	354	2	US-09-124-807-24	Sequence 24, Appl
34	51	89.5	357	2	US-09-984-292-7	Sequence 7, Appl
35	50	87.7	11	2	US-09-489-156-39	Sequence 39, Appl
36	50	87.7	13	2	US-09-489-156-18	Sequence 18, Appl
37	50	87.7	295	2	US-09-949-016-10678	Sequence 10678, A
38	50	87.7	354	2	US-09-949-016-6727	Sequence 6727, Ap
39	46	80.7	353	2	US-09-984-292-6	Sequence 6, Appl
40	46	80.7	353	2	US-09-984-292-18	Sequence 18, Appl
41	46	80.7	353	2	US-09-984-292-19	Sequence 19, Appl
42	46	80.7	359	2	US-09-984-292-12	Sequence 12, Appl
43	46	80.7	359	2	US-09-984-292-13	Sequence 13, Appl
44	46	80.7	359	2	US-09-984-292-22	Sequence 22, Appl
45	46	80.7	359	2	US-09-984-292-23	Sequence 23, Appl
46	41	71.9	11	1	US-08-019-073-26	Sequence 26, Appl
47	41	71.9	11	5	PCT-US94-01768-26	Sequence 26, Appl
48	41	71.9	15	1	US-08-019-073-3	Sequence 3, Appl
49	41	71.9	15	1	US-08-019-073-20	Sequence 20, Appl
50	41	71.9	15	1	US-08-019-073-21	Sequence 21, Appl
51	41	71.9	15	5	PCT-US94-01768-3	Sequence 3, Appl
52	41	71.9	15	5	PCT-US94-01768-20	Sequence 20, Appl
53	41	71.9	15	5	PCT-US94-01768-21	Sequence 21, Appl
54	41	71.9	24	1	US-08-019-073-4	Sequence 4, Appl
55	41	71.9	24	5	PCT-US94-01768-4	Sequence 4, Appl
56	40	70.2	154	2	US-09-270-767-32429	Sequence 32429, A
57	40	70.2	154	2	US-09-270-767-47646	Sequence 47646, A
58	39	68.4	10	7	5428134-4	Patent No. 5428134
59	39	68.4	10	7	5436320-4	Patent No. 5436320
60	39	68.4	13	2	US-09-489-156-20	Sequence 20, Appl
61	39	68.4	354	2	US-09-949-016-7936	Sequence 7936, Ap
62	39	68.4	906	2	US-08-630-316A-48	Sequence 48, Appl
63	38	66.7	207	2	US-09-270-767-32417	Sequence 32417, A
64	38	66.7	527	2	US-09-489-039A-10883	Sequence 10883, A
65	38	66.7	717	2	US-09-949-016-9436	Sequence 9436, Ap
66	38	66.7	1112	2	US-09-949-016-6891	Sequence 6891, Ap
67	38	66.7	1113	2	US-09-949-016-9904	Sequence 9904, Ap
68	37.5	65.8	477	2	US-09-004-838-46	Sequence 46, Appl
69	37.5	65.8	477	2	US-09-004-838-99	Sequence 99, Appl
70	37	64.9	15	1	US-08-019-073-5	Sequence 5, Appl
71	37	64.9	15	5	PCT-US94-01768-5	Sequence 5, Appl
72	37	64.9	24	1	US-08-019-073-6	Sequence 6, Appl
73	37	64.9	24	5	PCT-US94-01768-6	Sequence 6, Appl
74	37	64.9	854	1	US-09-070-060-4	Sequence 4, Appl
75	37	64.9	854	2	US-09-357-746-4	Sequence 4, Appl
76	37	64.9	885	2	US-09-248-796A-14427	Sequence 14427, A
77	36	63.2	174	2	US-09-270-767-37964	Sequence 37964, A
78	36	63.2	174	2	US-09-270-767-53181	Sequence 53181, A
79	36	63.2	270	2	US-09-107-532A-5444	Sequence 5444, Ap
80	36	63.2	358	2	US-09-438-917-19	Sequence 19, Appl
81	36	63.2	429	2	US-09-438-917-16	Sequence 16, Appl
82	36	63.2	473	2	US-09-438-917-6	Sequence 6, Appl
83	36	63.2	683	2	US-08-630-316A-46	Sequence 46, Appl
84	35	61.4	266	2	US-09-393-634-15	Sequence 15, Appl
85	35	61.4	302	2	US-09-248-796A-16913	Sequence 16913, A
86	35	61.4	312	3	US-10-770-127-109	Sequence 109, App
87	35	61.4	465	2	US-09-328-352-5222	Sequence 5222, Ap
88	35	61.4	568	2	US-09-628-966-10	Sequence 10, Appl
89	35	61.4	739	2	US-09-134-001C-3586	Sequence 3586, Ap
90	34	59.6	15	1	US-08-019-073-2	Sequence 2, Appl
91	34	59.6	15	1	US-08-019-073-31	Sequence 31, Appl
92	34	59.6	15	5	PCT-US94-01768-2	Sequence 2, Appl
93	34	59.6	15	5	PCT-US94-01768-31	Sequence 31, Appl
94	34	59.6	24	1	US-08-019-073-32	Sequence 32, Appl
95	34	59.6	24	5	PCT-US94-01768-32	Sequence 32, Appl
96	34	59.6	79	2	US-09-662-254B-21	Sequence 21, Appl
97	34	59.6	117	2	US-09-270-767-46230	Sequence 46230, A
98	34	59.6	117	2	US-09-270-767-61797	Sequence 61797, A
99	34	59.6	142	2	US-09-380-882-8	Sequence 8, Appl

100 34 59.6 225 2 US-09-489-039A-11585 Sequence 11585, A

## ALIGNMENTS

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RESULT 1
US-08-019-073-19
; Sequence 19, Application US/08019073
; Patent No. 5559209
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuro
; TITLE OF INVENTION: REGULATOR REGIONS OF G
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/019,073
; FILING DATE: 19930218
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/146001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-019-073-19

Query Match 100.0%; Score 57; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10
Db 1 KNNLKDCGLF 10

RESULT 2
US-08-429-964-50
; Sequence 50, Application US/08429964
; Patent No. 5962243
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: REISS, YUVAL
; APPLICANT: JAMES, GUY L.
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
; TITLE OF INVENTION: TRANSFERASE INHIBITORS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
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; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,964
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,625
; FILING DATE: 16-FEB-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/822,011
; FILING DATE: ABANDONED
; CLASSIFICATION: 435
; APPLICATION NUMBER: PCT/US/91/02650
; FILING DATE: 18-APR-1991
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/615,715
; FILING DATE: 20-NOV-1990
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/510,706
; FILING DATE: 18-APR-1990 (ABANDONED)
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, DAVID L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:432/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-429-964-50

Query Match 100.0%; Score 57; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10
Db 1 KNNLKDCGLF 10

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; Sequence 50, Application PC/TUS9308062
; GENERAL INFORMATION:
; APPLICANT:
; SEQUENCE CHARACTERISTICS:
; SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.
; SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.
; SEQUENCE CHARACTERISTICS: REISS, YUVAL
; SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.
; ADDRESSEE: METHODS AND COMPOSITIONS FOR
; ADDRESSEE: THE IDENTIFICATION,
; ADDRESSEE: CHARACTERIZATION AND
; ADDRESSEE: INHIBITION OF
; ADDRESSEE: FARNESYLTRANSFERASE
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
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Title: US-10-009-809-2

Perfect score: 57

Sequence: 1 KNNLKDCGLF 10

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	57	100.0	11	3	US-09-852-910-17
3	57	100.0	11	3	US-10-411-336A-17
4	57	100.0	13	3	US-09-852-910-112
5	57	100.0	13	4	US-10-373-540-16
6	57	100.0	13	4	US-10-411-336A-112
7	57	100.0	13	4	US-10-732-923-7631
8	57	100.0	13	5	US-10-732-923-8027
9	57	100.0	24	5	US-10-732-923-8053
10	57	100.0	301	5	US-10-732-923-7893
11	57	100.0	325	5	US-10-732-923-7981
12	57	100.0	333	5	US-10-732-923-7601
13	57	100.0	339	4	US-10-108-260A-3642
14	57	100.0	339	4	US-10-108-260A-3821
15	57	100.0	339	5	US-10-732-923-7893
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17	57	100.0	347	5	US-10-732-923-7991
18	57	100.0	349	5	US-10-732-923-7977
19	57	100.0	349	4	US-10-059-266B-18
20	57	100.0	353	4	US-10-732-923-7636
21	57	100.0	353	5	US-10-732-923-7637
22	57	100.0	353	5	US-10-732-923-7638
23	57	100.0	353	3	US-10-732-923-7661
24	57	100.0	354	3	US-09-952-680A-19
25	57	100.0	354	4	US-10-352-843-14
26	57	100.0	354	4	US-10-059-266B-4
27	57	100.0	354	5	US-10-215-982-19

28	57	100.0	354	5	US-10-732-923-7635	Sequence 7635, Ap
29	57	100.0	354	5	US-10-732-923-7663	Sequence 7663, Ap
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31	57	100.0	354	5	US-10-732-923-7686	Sequence 7686, Ap
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35	57	100.0	354	5	US-10-732-923-7925	Sequence 7925, Ap
36	57	100.0	354	5	US-10-732-923-7926	Sequence 7926, Ap
37	57	100.0	354	5	US-10-732-923-7933	Sequence 7933, Ap
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41	57	100.0	354	5	US-10-732-923-7975	Sequence 7975, Ap
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43	57	100.0	354	5	US-10-732-923-8043	Sequence 8043, Ap
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46	57	100.0	355	3	US-09-952-680A-23	Sequence 23, Appli
47	57	100.0	355	4	US-10-116-275-267	Sequence 267, App
48	57	100.0	355	4	US-10-408-765A-427	Sequence 427, App
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50	57	100.0	355	5	US-10-215-982-20	Sequence 20, Appli
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53	57	100.0	355	5	US-10-855-899-10	Sequence 10, Appli
54	57	100.0	355	5	US-10-855-805-10	Sequence 10, Appli
55	57	100.0	355	5	US-10-732-923-7598	Sequence 7598, Ap
56	57	100.0	355	5	US-10-732-923-7599	Sequence 7599, Ap
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61	57	100.0	355	5	US-10-732-923-7938	Sequence 7938, Ap
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67	57	100.0	355	5	US-10-732-923-8035	Sequence 8035, Ap
68	57	100.0	357	5	US-10-732-923-7678	Sequence 7678, Ap
69	57	100.0	377	5	US-10-732-923-7940	Sequence 7940, Ap
70	57	100.0	408	5	US-10-821-234-1100	Sequence 1100, Ap
71	57	100.0	695	5	US-10-491-654-23	Sequence 23, Appli
72	57	100.0	709	3	US-09-826-509-589	Sequence 589, App
73	57	100.0	709	3	US-10-925-095-589	Sequence 589, App
74	53	93.0	10	4	US-10-465-826-4	Sequence 4, Appli
75	53	93.0	26	4	US-10-465-826-10	Sequence 10, Appli
76	53	93.0	26	4	US-10-465-826-19	Sequence 19, Appli
77	51	89.5	10	4	US-10-465-826-2	Sequence 2, Appli
78	51	89.5	11	3	US-09-789-996-7	Sequence 7, Appli
79	51	89.5	11	3	US-09-852-910-15	Sequence 15, Appli
80	51	89.5	11	4	US-10-411-336A-15	Sequence 15, Appli
81	51	89.5	13	4	US-10-373-540-15	Sequence 15, Appli
82	51	89.5	26	4	US-10-465-826-25	Sequence 25, Appli
83	51	89.5	40	3	US-09-789-996-3	Sequence 3, Appli
84	51	89.5	157	3	US-09-952-680A-33	Sequence 33, Appli
85	51	89.5	157	3	US-10-215-982-33	Sequence 33, Appli
86	51	89.5	157	5	US-10-732-923-7626	Sequence 7626, Ap
87	51	89.5	167	5	US-10-732-923-7627	Sequence 7627, Ap
88	51	89.5	324	5	US-10-732-923-8046	Sequence 8046, Ap
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91	51	89.5	350	3	US-09-789-996-23	Sequence 23, Appli
92	51	89.5	350	3	US-09-952-680A-24	Sequence 24, Appli
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96	51	89.5	350	4	US-10-408-765A-428	Sequence 428, App
97	51	89.5	350	5	US-10-215-982-24	Sequence 24, Appli
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99	51	89.5	350	5	US-10-732-923-7716	Sequence 7716, Ap
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## ALIGNMENTS

RESULT 1  
US-10-465-826-31  
; Sequence 31, Application US/10465826  
; Publication No. US20040137006A1  
; GENERAL INFORMATION:  
; APPLICANT: ALLERGENE LTD.  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamir  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: ALL/002 US  
; CURRENT APPLICATION NUMBER: US/10/465,826  
; CURRENT FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-465-826-31

Query Match 100.0%; Score 57; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10  
Db 1 KNNLKDCGLF 10

RESULT 2  
US-09-852-910-17  
; Sequence 17, Application US/09852910  
; Publication No. US20030096297A1  
; GENERAL INFORMATION:  
; APPLICANT: Hamm, Heidi  
; APPLICANT: Gilchrist, Annette  
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor S  
; FILE REFERENCE: 2661-101  
; CURRENT APPLICATION NUMBER: US/09/852,910  
; CURRENT FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US 60/275,472  
; PRIOR FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 271  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-852-910-17

Query Match 100.0%; Score 57; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.002;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 KNNLKDCGLF 11

RESULT 3  
US-10-411-336A-17  
; Sequence 17, Application US/10411336A  
; Publication No. US20040018559A1  
; GENERAL INFORMATION:  
; APPLICANT: GILCHRIST, ANNETTE  
; APPLICANT: HAMM, HEIDI

; TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR  
; TITLE OF INVENTION: SIGNALING  
; FILE REFERENCE: 2661-102  
; CURRENT APPLICATION NUMBER: US/10/411,336A  
; CURRENT FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: US 09/852910  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: US 60/275472  
; PRIOR FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-411-336A-17

Query Match 100.0%; Score 57; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.002;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 KNNLKDCGLF 11

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US-09-852-910-112  
; Sequence 112, Application US/09852910  
; Publication No. US20030096297A1  
; GENERAL INFORMATION:  
; APPLICANT: Hamm, Heidi  
; APPLICANT: Gilchrist, Annette  
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor S  
; FILE REFERENCE: 2661-101  
; CURRENT APPLICATION NUMBER: US/09/852,910  
; CURRENT FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US 60/275,472  
; PRIOR FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 271  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 112  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(13)  
; OTHER INFORMATION: G alpha i minigene peptide  
US-09-852-910-112

Query Match 100.0%; Score 57; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0024;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10  
Db 4 KNNLKDCGLF 13

RESULT 5  
US-10-373-540-16  
; Sequence 16, Application US/10373540  
; Publication No. US20030162258A1  
; GENERAL INFORMATION:  
; APPLICANT: HAMM, HEIDI  
; APPLICANT: GILCHRIST, Annette  
; TITLE OF INVENTION: INHIBITORS OF G PROTEIN-MEDIATED SIGNALING, METHODS OF MAKING THEN  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 0290-29 (NU 95037)  
; CURRENT APPLICATION NUMBER: US/10/373,540  
; CURRENT FILING DATE: 2003-02-24  
; PRIOR APPLICATION NUMBER: US/09/489,156

GenCore version 5.1.9  
 Copyright (c) 1993 - 2006 Biocolloration Ltd.  
 OM protein - protein search, using sw model  
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Title: US-10-009-809-2

Perfect score: 57

Sequence: 1 KNNLKDCGLF 10

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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	53	93.0	26	7	US-11-214-588-10
6	53	93.0	26	7	US-11-214-588-19
7	51	89.5	10	7	US-11-214-588-2
8	51	89.5	26	7	US-11-214-588-25
9	50	87.7	10	7	US-11-214-588-1
10	50	87.7	10	7	US-11-214-588-3
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14	50	87.7	26	7	US-11-214-588-15
15	50	87.7	26	7	US-11-214-588-23
16	50	87.7	26	7	US-11-214-588-24
17	50	87.7	26	7	US-11-214-588-26
18	50	87.7	26	7	US-11-214-588-29
19	45	78.9	10	7	US-11-214-588-6
20	45	78.9	26	7	US-11-214-588-16
21	44	77.2	10	7	US-11-214-588-5
22	44	77.2	10	7	US-11-214-588-8
23	44	77.2	26	7	US-11-214-588-11
24	44	77.2	26	7	US-11-214-588-17
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27	70.2	40	10	7	US-11-214-588-7	Sequence 7, Appl
28	70.2	40	10	7	US-11-214-588-32	Sequence 32, Appl
29	70.2	40	26	7	US-11-214-588-12	Sequence 12, Appl
30	70.2	40	26	7	US-11-214-588-21	Sequence 21, Appl
31	70.2	40	26	7	US-11-214-588-30	Sequence 30, Appl
32	70.2	40	26	7	US-11-214-588-30	Sequence 30, Appl
33	70.2	40	26	7	US-11-214-588-30	Sequence 30, Appl
34	70.2	40	26	7	US-11-214-588-30	Sequence 30, Appl
35	66.7	38	468	6	US-10-953-349-23329	Sequence 23329, A
36	66.7	38	468	6	US-10-953-349-23329	Sequence 23329, A
37	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
38	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
39	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
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41	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
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44	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
45	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
46	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
47	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
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50	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
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69	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
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81	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
82	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
83	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
84	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
85	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
86	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
87	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
88	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
89	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
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92	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
93	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
94	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
95	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
96	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
97	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap
98	61.4	35	213	7	US-11-174-307B-4516	Sequence 4516, Ap

99 31 54.4 386 6 US-10-953-349-23720 Sequence 23720, A  
100 31 54.4 402 6 US-10-953-349-7103 Sequence 7103, Ap

## ALIGNMENTS

RESULT 1  
US-11-214-588-31  
; Sequence 31, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-214-588-31

Query Match 100.0%; Score 57; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.7e-05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10  
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Db 1 KNNLKDCGLF 10

RESULT 2  
US-11-293-697-3642  
; Sequence 3642, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3642  
; LENGTH: 339  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-3642

Query Match 100.0%; Score 57; DB 7; Length 339;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10  
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Db 330 KNNLKDCGLF 339

RESULT 3  
US-11-293-697-3821  
; Sequence 3821, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3821  
; LENGTH: 339  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-3821

Query Match 100.0%; Score 57; DB 7; Length 339;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10  
|||||  
Db 330 KNNLKDCGLF 339

RESULT 4  
US-11-214-588-4  
; Sequence 4, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (10)-(10)  
; OTHER INFORMATION: Para-amino Phenylalanine at position 10  
US-11-214-588-4

Query Match 93.0%; Score 53; DB 7; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.00047;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10  
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Db 1 KNNLKDCGLF 10

RESULT 5  
US-11-214-588-10  
; Sequence 10, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:50:59 ; Search time 4.83871 Seconds  
(without alignments)  
198.848 Million cell updates/sec

Title: US-10-009-809-2

Perfect score: 57

Sequence: 1 KNNLKDCGLF 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	354	1 RGH011	GTP-binding regula
2	57	100.0	354	1 RGH011	GTP-binding regula
3	57	100.0	354	1 RGH011	GTP-binding regula
4	57	100.0	354	1 RGH011	GTP-binding regula
5	57	100.0	354	2 S28157	GTP-binding regula
6	57	100.0	354	2 S24362	GTP-binding regula
7	57	100.0	354	2 I50237	GTP-binding regula
8	57	100.0	354	2 S27013	GTP-binding regula
9	57	100.0	355	1 RGH012	GTP-binding regula
10	57	100.0	355	1 RGH012	GTP-binding regula
11	57	100.0	355	1 RGH012	GTP-binding regula
12	57	100.0	355	2 S28158	GTP-binding regula
13	57	100.0	355	2 I50238	GTP-binding regula
14	57	100.0	355	2 A61031	GTP-binding regula
15	57	100.0	355	2 A48976	GTP-binding regula
16	51	89.5	350	1 RGH011	GTP-binding regula
17	51	89.5	350	1 RGH011	GTP-binding regula
18	51	89.5	350	1 RGH011	GTP-binding regula
19	51	89.5	354	1 RGH012	GTP-binding regula
20	51	89.5	354	1 RGH012	GTP-binding regula
21	51	89.5	354	2 S24352	GTP-binding regula
22	50	87.7	63	2 I48071	GTP-binding regula
23	50	87.7	354	1 RGH013	GTP-binding regula
24	50	87.7	354	1 RGH013	GTP-binding regula
25	50	87.7	354	2 S28159	GTP-binding regula
26	50	87.7	354	2 S40508	GTP-binding regula
27	50	87.7	354	2 S40509	GTP-binding regula
28	49	86.0	104	2 B25888	GTP-binding regula
29	41	71.9	355	1 RGH011	GTP-binding regula

30	40	70.2	394	2	B69619	phosphodeoxyribom
31	39	68.4	345	1	RGXLI3	GTP-binding regula
32	39	68.4	354	1	RGH011	GTP-binding regula
33	39	68.4	354	1	RGH011	GTP-binding regula
34	39	68.4	354	1	RGH011	GTP-binding regula
35	39	68.4	354	1	RGH011	GTP-binding regula
36	39	68.4	354	1	RGH011	GTP-binding regula
37	39	68.4	354	1	RGH011	GTP-binding regula
38	39	68.4	354	1	RGH011	GTP-binding regula
39	39	68.4	354	1	RGH011	GTP-binding regula
40	39	68.4	354	1	RGH011	GTP-binding regula
41	39	68.4	354	1	RGH011	GTP-binding regula
42	39	68.4	472	1	T10889	1-aminocyclopropan
43	39	68.4	778	2	C71944	hypothetical prote
44	38	66.7	480	2	T26614	hypothetical prote
45	38	66.7	1240	2	T48800	SMT4 related prote
46	38	66.7	1627	2	S65464	pregnancy-associat
47	37	64.9	347	1	QOCV51	Alu protein - squa
48	37	64.9	4550	2	T18440	hypothetical prote
49	37	64.9	5825	2	T12117	polypeptide - fava
50	36.5	64.0	55	2	A82464	hypothetical prote
51	36	63.2	226	2	C81328	hypothetical prote
52	36	63.2	238	2	S49400	H+-transporting tw
53	36	63.2	345	2	T29786	hypothetical prote
54	36	63.2	445	2	T19611	hypothetical prote
55	36	63.2	473	2	JC7359	splicing factor, S
56	36	63.2	483	2	T26613	hypothetical prote
57	36	63.2	490	2	T24497	hypothetical prote
58	36	63.2	495	2	AH0985	probable zinc-prot
59	35	61.4	83	2	B84494	hypothetical prote
60	35	61.4	151	2	E97107	ferric uptake regu
61	35	61.4	206	2	I53735	nerve terminal pro
62	35	61.4	249	2	S38308	SNAP-25 protein -
63	35	61.4	296	2	G87611	branched-chain ami
64	35	61.4	301	2	H90179	conserved hypothet
65	35	61.4	367	2	AE3303	putrescine-binding
66	35	61.4	371	2	T08759	conserved hypothet
67	35	61.4	412	2	H81415	probable molybdenu
68	35	61.4	497	2	S47890	xuperantia 1 - fr
69	35	61.4	553	2	T02475	hypothetical prote
70	35	61.4	671	2	D84648	probable disease r
71	35	61.4	2539	2	B71619	hypothetical prote
72	34	59.6	142	2	JT0573	retinoic acid-indu
73	34	59.6	149	2	E41317	probable lipopolys
74	34	59.6	210	2	B84943	DNA-(apurinic or a
75	34	59.6	232	2	AB0973	lipopolysaccharide
76	34	59.6	303	2	A84114	glycosyltransferas
77	34	59.6	331	2	G83876	hypothetical prote
78	34	59.6	335	2	T40160	conserved hypothet
79	34	59.6	358	2	T02383	hypothetical prote
80	34	59.6	373	2	T33145	hypothetical prote
81	34	59.6	374	2	A71803	probable regulator
82	34	59.6	386	2	T28176	hypothetical prote
83	34	59.6	433	2	T48320	hypothetical prote
84	34	59.6	526	2	G83436	hypothetical prote
85	34	59.6	571	2	B86150	hypothetical prote
86	34	59.6	608	2	T10906	starch synthase (E
87	34	59.6	633	2	F97834	hypothetical prote
88	34	59.6	652	2	T37822	probable centromer
89	34	59.6	778	2	A64656	hypothetical prote
90	34	59.6	869	2	F97126	mismatch repair pr
91	34	59.6	904	1	RGH011	regulatory protein
92	34	59.6	912	2	T18785	hypothetical prote
93	34	59.6	920	2	T26650	hypothetical prote
94	34	59.6	1143	2	A69465	DNA-directed DNA p
95	34	59.6	1650	2	T18444	hypothetical prote
96	34	59.6	2168	2	D88131	protein F10G7.10 [
97	33	57.9	131	2	C97216	nimC/Nima family p
98	33	57.9	135	2	S49200	cytochrome b5 - co
99	33	57.9	135	2	AC2171	hypothetical prote
100	33	57.9	135	2	S46306	cytochrome b5 - co

## ALIGNMENTS

## RESULT 1

RG9011  
 GTP-binding regulatory protein Gi alpha-1 chain (adenylate cyclase-inhibiting) - bovine  
 N;Alternate names: guanine nucleotide binding protein Gi alpha-1 chain; heterotrimeric G  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004  
 A;Accession: A23631; A25888  
 R;Nukada, T.; Tanabe, T.; Takahashi, H.; Noda, M.; Haga, K.; Haga, T.; Ichiyama, A.; Kar  
 FEBS Lett. 197, 305-310, 1986  
 A;Title: Primary structure of the alpha-subunit of bovine adenylate cyclase-inhibiting G  
 A;Reference number: A23631; MUID:86136587; PMID:2419165  
 A;Accession: A23631  
 A;Molecule type: mRNA  
 A;Residues: 1-354 <NUN>  
 A;Cross-references: UNIPROT:P04898; UNIPARC:UPI00000124A; GB:X03642; NID:G3390; PIDN:CA  
 R;Michel, T.; Winslow, J.W.; Smith, J.A.; Seidman, J.G.; Neer, E.J.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 7663-7667, 1986  
 A;Title: Molecular cloning and characterization of cDNA encoding the GTP-binding protein  
 A;Reference number: A94131; MUID:87017009; PMID:3094012  
 A;Accession: A25888  
 A;Molecule type: mRNA  
 A;Residues: 106-112, 'S', 114-329, 'N', 331-336, 'E', 338-354 <MIC>  
 A;Cross-references: UNIPARC:UPI000015C31B; GB:M14207; NID:G163129; PIDN:AAA30561.1; PID:  
 C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay  
 ains. The beta and gamma chains, required for GTPase activity, appear to be common to al  
 rase; it is specific for each type of G protein.  
 C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal reg  
 C;Superfamily: GTP-binding regulatory protein Gs alpha chain  
 C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; nu  
 F;2-354/Product: GTP-binding regulatory protein Gi alpha-1 chain #status predicted <MAT>  
 F;40-47/Region: nucleotide-binding motif A (P-loop)  
 F;269-272/Region: GTP-binding NKXD motif  
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F;3/Binding site: palmitate (Cys) (covalent) #status predicted  
 F;178/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted  
 F;351/Modified site: ADP-ribosylcysteine (Cys) (by pertussis toxin) #status predicted  
 Query Match 100.0%; Score 57; DB 1; Length 354;  
 Best Local Similarity 100.0%; Pred. No. 0.0095;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KNNLKDCGLF 10  
 |||||  
 Db 345 KNNLKDCGLF 354

RESULT 2  
 RG9011  
 GTP-binding regulatory protein Gi alpha-1 chain (adenylate cyclase-inhibiting) - human  
 N;Alternate names: guanine nucleotide binding protein Gi alpha-1 chain; heterotrimeric G  
 C;Species: Homo sapiens (man)  
 C;Date: 31-Dec-1992 #sequence\_revision 22-Nov-1996 #text\_change 09-Jul-2004  
 A;Accession: A28318; D28154; T08669  
 R;Bray, P.; Carter, A.; Guo, V.; Puckett, C.; Kamholz, J.; Spiegel, A.; Nirenberg, M.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 5115-5119, 1987  
 A;Title: Human cDNA clones for an alpha subunit of Gi signal-transduction protein.  
 A;Reference number: A28318; MUID:87260939; PMID:3110783  
 A;Accession: A28318  
 A;Molecule type: mRNA  
 A;Residues: 6-354 <BRA>  
 A;Cross-references: UNIPROT:P04898; UNIPARC:UPI000016A9C6; GB:M17219; NID:G183410; PIDN:  
 R;Itoh, H.; Toyama, R.; Kozasa, T.; Tsukamoto, T.; Matsuo, M.; Kazi, Y.  
 J. Biol. Chem. 263, 6656-6664, 1988  
 A;Title: Presence of three distinct molecular species of G-i protein alpha-subunit. Stru  
 A;Reference number: A28154; MUID:88198230; PMID:2834384  
 A;Accession: D28154  
 A;Status: not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-101 <ITO>  
 A;Cross-references: UNIPARC:UPI000016A99A; GB:M20596; GB:M19476; NID:G183189; PIDN:AAA35

R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gaseenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, March 1999  
 A;Reference number: Z16467  
 A;Accession: T08669

A;Molecule type: mRNA  
 A;Residues: 'WGCSAATGSSAAATVPRDSKTPOTRDLGALSRAKQSLVVRNSRPLLSAPLRTASPTPLRKWGRGPRREAF  
 A;Cross-references: UNIPARC:UPI00001740E7; EMBL:AL049933  
 A;Experimental source: fetal brain; clone DKFp564K1216  
 A;Note: differences are due to different assignment of start codons  
 C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay  
 ains. The beta and gamma chains, required for GTPase activity, appear to be common to all  
 rase; it is specific for each type of G protein.  
 C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal reg  
 C;Genetics:  
 A;Gene: GDB:GNAIL  
 A;Cross-references: GDB:120001; OMIM:139310  
 A;Map position: 7q21-7q21  
 A;Note: DKFp564K1216.1  
 C;Superfamily: GTP-binding regulatory protein Gs alpha chain  
 C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; nu  
 F;2-354/Product: GTP-binding regulatory protein Gi alpha-1 chain #status predicted <MAT>  
 F;40-47/Region: nucleotide-binding motif A (P-loop)  
 F;269-272/Region: GTP-binding NKXD motif  
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F;3/Binding site: palmitate (Cys) (covalent) #status predicted  
 F;178/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted  
 F;351/Modified site: ADP-ribosylcysteine (Cys) (by pertussis toxin) #status predicted  
 Query Match 100.0%; Score 57; DB 1; Length 354;  
 Best Local Similarity 100.0%; Pred. No. 0.0095;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KNNLKDCGLF 10  
 |||||  
 Db 345 KNNLKDCGLF 354

RESULT 3  
 RG9011  
 GTP-binding regulatory protein Gi alpha-1 chain (adenylate cyclase-inhibiting) - rat  
 N;Alternate names: guanine nucleotide binding protein Gi alpha-1 chain; heterotrimeric G  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004  
 A;Accession: C27423  
 R;Jones, D.T.; Reed, R.R.  
 J. Biol. Chem. 262, 14241-14249, 1987  
 A;Title: Molecular cloning of five GTP-binding protein cDNA species from rat olfactory ne  
 A;Reference number: A92614; MUID:88007678; PMID:2820999  
 A;Accession: C27423  
 A;Molecule type: mRNA  
 A;Residues: 1-354 <JON>  
 A;Cross-references: UNIPROT:P10824; UNIPARC:UPI0000167A2B; GB:M17527; NID:G203167; PIDN:  
 C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay  
 ains. The beta and gamma chains, required for GTPase activity, appear to be common to all  
 rase; it is specific for each type of G protein.  
 C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal reg  
 C;Superfamily: GTP-binding regulatory protein Gs alpha chain  
 C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; nu  
 F;2-354/Product: GTP-binding regulatory protein Gi alpha-1 chain #status predicted <MAT>  
 F;40-47/Region: nucleotide-binding motif A (P-loop)  
 F;269-272/Region: GTP-binding NKXD motif  
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F;3/Binding site: palmitate (Cys) (covalent) #status predicted  
 F;178/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted  
 F;351/Modified site: ADP-ribosylcysteine (Cys) (by pertussis toxin) #status predicted  
 Query Match 100.0%; Score 57; DB 1; Length 354;  
 Best Local Similarity 100.0%; Pred. No. 0.0095;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KNNLKDCGLF 10  
 |||||  
 Db 345 KNNLKDCGLF 354



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:50:27 ; Search time 36.9355 Seconds  
(without alignments)  
250.441 Million cell updates/sec

Title: US-10-009-809-2

Perfect score: 57

Sequence: 1 KNNLKDCGLF 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt\_7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	53	2 Q922Y6	MUS MUSCULU
2	57	100.0	132	2 Q8JZT4	MOUSE
3	57	100.0	157	2 Q6LCB5	HUMAN
4	57	100.0	301	2 Q9Y206	HYDRA MAGNI
5	57	100.0	347	2 Q7ZW15	BRARE
6	57	100.0	353	1 GNAI1	BOVIN
7	57	100.0	353	1 GNAI1	CHICK
8	57	100.0	353	1 GNAI1	HUMAN
9	57	100.0	353	1 GNAI1	ORLYA
10	57	100.0	353	1 GNAI1	PONPY
11	57	100.0	353	1 GNAI1	RAT
12	57	100.0	353	1 GNAI1	XENLA
13	57	100.0	353	1 GNAI1	XENLA
14	57	100.0	353	1 GNAI1	ASTPE
15	57	100.0	353	1 GNAI1	HELT
16	57	100.0	353	1 GNAI1	LYMST
17	57	100.0	353	2 Q5DEN1	SCHJA
18	57	100.0	353	2 Q7Q6E0	ANOGE
19	57	100.0	353	2 Q5R9N4	PONPY
20	57	100.0	354	1 GNAI2	CAVPO
21	57	100.0	354	1 GNAI2	CAVPO
22	57	100.0	354	1 GNAI2	CHICK
23	57	100.0	354	1 GNAI2	HUMAN
24	57	100.0	354	1 GNAI2	MACFA
25	57	100.0	354	1 GNAI2	MOUSE
26	57	100.0	354	1 GNAI2	ORLYA
27	57	100.0	354	1 GNAI2	RAT
28	57	100.0	354	1 GNAI1	HOMAM
29	57	100.0	354	2 Q6QMI6	LYTVA
30	57	100.0	354	2 Q6QMI7	STRPU
31	57	100.0	354	2 Q8WP45	HALRO

32	57	100.0	354	2 Q8WSS1	CIOIN
33	57	100.0	354	2 Q8WSS2	CIOIN
34	57	100.0	354	2 Q9NL94	OCTVU
35	57	100.0	354	2 Q2KJC0	BOVIN
36	57	100.0	354	2 Q3LRD4	CRIGR
37	57	100.0	354	2 Q45QN2	RAT
38	57	100.0	354	2 Q4S7I0	TETNG
39	57	100.0	354	2 Q6GPC5	XENLA
40	57	100.0	354	2 Q7T3D3	BRARE
41	57	100.0	355	2 Q96C71	HUMAN
42	57	100.0	355	2 Q3HR13	CRIGR
43	57	100.0	355	2 Q3TXK7	MOUSE
44	57	100.0	355	2 Q45QN0	RAT
45	57	100.0	355	2 Q5U4X0	XENLA
46	57	100.0	355	2 Q6P3M7	XENLA
47	57	100.0	355	2 Q6TNT8	BRARE
48	57	100.0	355	2 Q9W6A4	SQUAC
49	57	100.0	377	2 Q7ZW82	BRARE
50	57	100.0	404	2 Q4SAC0	TETNG
51	57	100.0	499	2 Q4RXT7	TETNG
52	54	94.7	82	2 Q8QV6	FUGRU
53	51	89.5	47	2 Q8QV9	FUGRU
54	51	89.5	157	2 Q8BSY7	MOUSE
55	51	89.5	222	2 Q4TH72	TETNG
56	51	89.5	336	2 Q4RVS6	TETNG
57	51	89.5	343	2 Q9D7B3	MOUSE
58	51	89.5	349	1 GNAI1	BOVIN
59	51	89.5	349	1 GNAI1	CANFA
60	51	89.5	349	1 GNAI1	HUMAN
61	51	89.5	349	1 GNAI1	MOUSE
62	51	89.5	349	1 GNAI1	XENLA
63	51	89.5	350	2 Q4VBN2	HUMAN
64	51	89.5	350	2 P79895	SPAUA
65	51	89.5	350	2 Q2T914	XENLA
66	51	89.5	350	2 Q4L222	GECE
67	51	89.5	350	2 Q4RJA7	TETNG
68	51	89.5	350	2 Q6DJF0	XENLA
69	51	89.5	350	2 Q90WX6	BRARE
70	51	89.5	350	2 Q9DG28	CHICK
71	51	89.5	350	2 Q9YI23	AMBTI
72	51	89.5	353	1 GNAI2	BOVIN
73	51	89.5	353	1 GNAI2	HUMAN
74	51	89.5	353	1 GNAI2	MOUSE
75	51	89.5	353	1 GNAI2	RAT
76	51	89.5	354	2 Q5T697	HUMAN
77	51	89.5	354	2 Q90WX5	BRARE
78	51	89.5	354	2 Q9DG27	CHICK
79	51	89.5	358	2 Q8QVY3	FUGRU
80	51	89.5	371	2 Q8QVY8	FUGRU
81	50	87.7	63	1 GNAI3	CRIGR
82	50	87.7	89	2 Q8QZ22	FUGRU
83	50	87.7	346	2 Q45QM8	RAT
84	50	87.7	353	1 GNAI3	CAVPO
85	50	87.7	353	1 GNAI3	HUMAN
86	50	87.7	353	1 GNAI3	MOUSE
87	50	87.7	353	1 GNAI3	RAT
88	50	87.7	354	2 Q5TZK1	HUMAN
89	50	87.7	354	2 Q3ZCA7	BOVIN
90	50	87.7	354	2 Q3HR12	CRIGR
91	50	87.7	354	2 Q3TGV1	MOUSE
92	50	87.7	354	2 Q3TJH1	MOUSE
93	50	87.7	354	2 Q90846	CHICK
94	50	87.7	354	2 Q90847	GALLUS
95	47	82.5	426	2 Q4RXB3	TETNG
96	46	80.7	358	1 GPA45	CABER
97	45	78.9	354	2 Q6DJF3	XENLA
98	45	78.9	354	2 Q9YI22	AMBTI
99	44	77.2	301	2 Q9YI27	9METZ
100	42	73.7	306	2 Q5L8N4	BACFN

ALIGNMENTS

```

RESULT 1
Q922Y6_MOUSE PRELIMINARY; PRT; 53 AA.
AC Q922Y6;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE 07-FEB-2006, entry version 19.
DE Gna12 protein (Fragment).
GN Name=Gna12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.; STRAIN=FVB/N;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. Metallothionien-TGF alpha model.
RC 10 month old virgin mouse. Taken by biopsy.;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC006695; AAH06695.1; -; mRNA.
DR HSSP; P10824; 1GDD.
DR SMR; Q922Y6; 1-53.
DR Ensemble; ENSMUSG000000032562; Mus musculus.
DR MGI; MGI:95772; Gna12.
DR GO; GO:0003924; F:GTPase activity; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0008283; P:cell proliferation; IPI.
DR GO; GO:0007213; P:acetylcholine receptor signaling, muscarini. . .; IMP.
DR GO; GO:0007193; P:G-protein signaling, IPI.
DR GO; GO:0007193; P:G-protein signaling, adenylyate cyclase inh. . .; IMP.
DR InterPro; IPR001019; G-protein_alph_bd.
DR Pfam; PF00503; G-alpha; 1.
DR SMART; SM00275; G_alpha; 1.
DR NONTER 1
FT
SQ SEQUENCE 53 AA; 6220 MW; 6574BE1F71B884E4 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10
DB 44 KNNLKDCGLF 53

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RESULT 2
Q8JZT4_MOUSE PRELIMINARY; PRT; 132 AA.
AC Q8JZT4;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DE 07-FEB-2006, entry version 20.
DE Gna12 protein.
GN Name=Gna12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC037130; AAH37130.1; -; mRNA.
DR HSSP; P10824; 1AGR.
DR SMR; Q8JZT4; 5-131.
DR Ensemble; ENSMUSG000000032562; Mus musculus.
DR MGI; MGI:95772; Gna12.
DR GO; GO:0003924; F:GTPase activity; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007213; P:acetylcholine receptor signaling, muscarini. . .; IMP.
DR GO; GO:0008283; P:cell proliferation; IPI.
DR GO; GO:0007193; P:G-protein signaling, IPI.
DR GO; GO:0007193; P:G-protein signaling, adenylyate cyclase inh. . .; IMP.
DR InterPro; IPR001019; G-protein_alph_bd.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00441; GPROTEINAI.
DR SMART; SM00275; G_alpha; 1.
DR NONTER 1
FT
SQ SEQUENCE 132 AA; 15289 MW; 064DCD1E011C3C4C CRC64;

Query Match 100.0%; Score 57; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10
DB 123 KNNLKDCGLF 132

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:50:22 ; Search time 65.0323 Seconds  
(without alignments)  
112.490 Million cell updates/sec

Title: US-10-009-809-3

Perfect score: 70

Sequence: 1 AAVALLPAVLLALLAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq\_8.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*
- 10: Geneseq2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	16	2	AAR87629
2	70	100.0	16	2	AAW37753
3	70	100.0	16	2	AAW56394
4	70	100.0	16	2	AAW48689
5	70	100.0	16	2	AAW53769
6	70	100.0	16	2	AAW13506
7	70	100.0	16	3	AAW67954
8	70	100.0	16	3	AAW55815
9	70	100.0	16	4	AAW02979
10	70	100.0	16	4	AAW97005
11	70	100.0	16	4	AAE11949
12	70	100.0	16	4	AAU03154
13	70	100.0	16	4	AAW72476
14	70	100.0	16	5	ABG78989
15	70	100.0	16	5	AAU10399
16	70	100.0	16	5	AAE15613
17	70	100.0	16	5	AAU78349
18	70	100.0	16	5	AAE26128
19	70	100.0	16	5	ABG75507
20	70	100.0	16	5	ABB81177
21	70	100.0	16	5	AAE23686
22	70	100.0	16	6	ABG82543
23	70	100.0	16	6	ABR84444

24	70	100.0	16	6	AAE33897	Aae33897	Kaposi's
25	70	100.0	16	6	ABU09984	Abu09984	Kaposi's
26	70	100.0	16	7	ADC22454	Adc22454	Protein-d
27	70	100.0	16	7	ADF78064	Adf78064	Human mem
28	70	100.0	16	7	ADG28017	Adg28017	Kaposi FG
29	70	100.0	16	7	ADH76184	Adh76184	Transduct
30	70	100.0	16	7	ADK11581	Adk11581	Taxoid ca
31	70	100.0	16	7	ADL88653	Adl88653	MPS (Kapo
32	70	100.0	16	8	ADG73832	Adg73832	Peptide d
33	70	100.0	16	8	ADH58870	Adh58870	Glutathio
34	70	100.0	16	8	ADJ78875	Adj78875	N-termina
35	70	100.0	16	8	ADL14686	Adl14686	Cardiant
36	70	100.0	16	8	ADK15574	Adk15574	Membrane
37	70	100.0	16	8	ADO26466	Ado26466	Kaposi's
38	70	100.0	16	8	ADM97016	Adm97016	Botulinum
39	70	100.0	16	8	ADO25265	Ado25265	Signal se
40	70	100.0	16	8	ADP08148	Adp08148	Small int
41	70	100.0	16	8	ADP08145	Adp08145	Small int
42	70	100.0	16	8	ADQ60179	Adq60179	Human her
43	70	100.0	16	8	ADR31972	Adr31972	Heat choc
44	70	100.0	16	8	ADR82252	Adr82252	Membrane
45	70	100.0	16	8	ADU15734	Adu15734	MUC1-PDZ
46	70	100.0	16	8	ADT61097	Adt61097	Novel int
47	70	100.0	16	8	ADU07192	Adu07192	Membrane
48	70	100.0	16	8	ADT61891	Adt61891	Human mem
49	70	100.0	16	8	ADT86673	Adt86673	Membrane
50	70	100.0	16	8	ADU67511	Adu67511	Membrane
51	70	100.0	16	8	ADU26590	Adu26590	Cell perm
52	70	100.0	16	8	ABE19669	Abe19669	Novel gen
53	70	100.0	16	9	ADW25982	Adw25982	Membrane
54	70	100.0	16	9	ADW81340	Adw81340	Intrabody
55	70	100.0	16	9	ADW88632	Adw88632	Membrane
56	70	100.0	16	9	ADY32269	Ady32269	Novel can
57	70	100.0	16	9	ADY38682	Ady38682	Novel pro
58	70	100.0	16	9	ADZ64558	Adz64558	Kaposi's
59	70	100.0	16	9	ADZ68062	Adz68062	Kaposi's
60	70	100.0	16	9	ADZ69395	Adz69395	HSP20 tra
61	70	100.0	16	9	AEA98089	Aea98089	Signal se
62	70	100.0	16	9	AEA33043	Aea33043	Kaposi fi
63	70	100.0	16	9	AEA36361	Aea36361	Basic dom
64	70	100.0	16	9	ABE17248	Abe17248	Human mem
65	70	100.0	16	9	AEA43032	Aea43032	Membrane
66	70	100.0	16	9	ABE28494	Abe28494	MPS (Kapo
67	70	100.0	16	9	AEC78139	Aec78139	NP3 der
68	70	100.0	16	9	AED02530	Aed02530	SN50 (NF-
69	70	100.0	16	9	AED51657	Aed51657	Cell perm
70	70	100.0	16	9	AED83101	Aed83101	Membrane
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73	70	100.0	16	10	AE91963	Aee91963	Kaposi FG
74	70	100.0	16	10	AE848449	Aee848449	Signal se
75	70	100.0	16	10	AEF42977	Aef42977	Kaposi fi
76	70	100.0	16	10	AEF90254	Aef90254	Signal se
77	70	100.0	16	10	AEF99409	Aef99409	Hydrophob
78	70	100.0	17	3	AAW67960	Aay67960	Kaposi s
79	70	100.0	17	3	AAW67961	Aay67961	Kaposi s
80	70	100.0	17	6	ABP56849	Abp56849	Peptide F
81	70	100.0	17	10	AEF93014	Aef93014	Caspase-9
82	70	100.0	18	4	AAE12490	Aae12490	Membrane
83	70	100.0	18	9	ABE09929	Abe09929	Antiviral
84	70	100.0	19	3	AAW67955	Aay67955	Kaposi s
85	70	100.0	19	3	AAW67956	Aay67956	Kaposi s
86	70	100.0	19	8	ADJ84000	Adj84000	Apoptosis
87	70	100.0	19	8	ADP74538	Adp74538	Caspase i
88	70	100.0	19	10	AEF93007	Aef93007	Caspase i
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95	70	100.0	20	5	AAO18582	Aao18582	Caspase-1
96	70	100.0	20	7	ADG98869	Adg98869	Caspase 8

97 70 100.0 20 7 ADG98866 Caspase 3  
 98 70 100.0 20 7 ADG98868 Caspase 6  
 99 70 100.0 20 7 ADG98867 Caspase 4  
 100 70 100.0 20 7 ADG98870 Caspase 9

## ALIGNMENTS

RESULT 1  
 AAR87629  
 ID AAR87629 standard; peptide; 16 AA.  
 AC AAR87629;  
 XX  
 XX 23-JUL-1996 (first entry)  
 XX  
 XX Signal peptide of K-FGF.  
 XX  
 XX Signal peptide; K-FGF; kaposi fibroblast growth factor; FGF; inhibition;  
 KW growth factor; nuclear localisation sequence; growth regulation; p50;  
 KW tumour cell; transcription factor; NF-kappaB; therapy.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9534295-A1.  
 PN  
 XX 21-DEC-1995.  
 PD  
 XX 13-JUN-1995; 95WO-US007539.  
 PF  
 XX 13-JUN-1994; 94US-00258852.  
 PR  
 XX (UYVA-) UNIV VANDERBILT.  
 PA  
 XX Lin Y, Hawiger JJ;  
 PI  
 XX WPI; 1996-049396/05.  
 DR

XX Importing biologically active molecules ex vivo or in vivo into cells -  
 PT useful in regulation of cell growth and inhibition of gene expression.  
 PT  
 PS Claim 5; Page 35; 47pp; English.

XX This sequence represents the signal peptide of Kaposi fibroblast growth  
 CC factor (K-FGF). This sequence is an importation competent signal peptide  
 CC (SP), and is used in the methods of the invention. These methods are  
 CC designed to import a biologically active molecule (BAM) into a cell  
 CC (either ex vivo or in vivo). The methods comprise administering to the  
 CC cell a complex comprising the BAM linked to an importation competent SP  
 CC (such as this sequence), and thereby importing the BAM into the cell. The  
 CC BAM-SP complex is optionally linked to a nuclear localisation sequence  
 CC peptide (NLS), to achieve importation into the nucleus of a cell. This  
 CC method can be used to regulate the growth of a cell, e.g. tumour cells.  
 CC Aleo, for inhibiting the expression of a gene. Genes regulated by a  
 CC transcription factor, such as NF-kappaB are inhibited by a complex  
 CC comprising an SP linked to an NLS of the active p50 subunit of NF-kappaB.  
 CC This method imports BAM's into a cell using mechanisms naturally occurring  
 CC in cells, thereby avoiding damaging the target cells. It can also be used  
 CC to import molecules into large numbers of cells, including organs

XX Sequence 16 AA;

Query Match 100.0%; Score 70; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.0008;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVALLPAVLLALLAP 16  
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 Db 1 AAVALLPAVLLALLAP 16

RESULT 2

AAW37753  
 ID AAW37753 standard; peptide; 16 AA.  
 XX  
 AC AAW37753;  
 XX  
 XX 20-JUL-1998 (first entry)  
 DT  
 XX Chimeric peptide 1.  
 DE  
 XX Chimeric peptide; signal peptide; ras gene product; mutation;  
 KW leukaemic cell; bone marrow cell; transduction.  
 KW  
 XX Synthetic.  
 OS  
 XX US5736394-A.  
 PN  
 XX 07-APR-1998.  
 PD  
 XX 03-MAY-1996; 96US-00642493.  
 PF  
 XX 03-MAY-1996; 96US-00642493.  
 PR  
 XX (BOST-) BOSTON BIOMEDICAL RES INST.  
 XX  
 XX Coleman PS, Sheldon K;  
 PI  
 XX WPI; 1998-239216/21.  
 DR  
 XX Cellular uptake of specific modified peptide(s) - useful for covalent  
 PT bonding to, and inactivation of intracellular proteins.  
 PT  
 XX Disclosure; Col 3; lipp; English.  
 PS  
 XX This amino acid sequence is of a chimeric peptide comprising a known  
 CC signal peptide, and is used in the method of invention as a way of  
 CC introducing a peptide into a cell. They are also useful for specifically  
 CC covalently binding a peptide to a target protein in a cell and  
 CC irreversibly block a binding site on the protein e.g. the peptide can be  
 CC used to inactivate the ras gene product which is mutated in leukaemic  
 CC cells and essential for survival, but not essential in normal bone marrow  
 CC cells. It can also be used to deduce the role of different proteins in  
 CC signal transduction pathways by systematically inactivating them and  
 CC seeing the resultant effects  
 CC  
 XX Sequence 16 AA;  
 SQ  
 Query Match 100.0%; Score 70; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.0008;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AAVALLPAVLLALLAP 16  
 |||||  
 Db 1 AAVALLPAVLLALLAP 16

RESULT 3  
 AAW56394  
 ID AAW56394 standard; peptide; 16 AA.  
 XX  
 AC AAW56394;  
 XX  
 XX 05-AUG-1998 (first entry)  
 DT  
 XX MEM polypeptide used to inhibit kappa-Ig light chain expression.  
 DE  
 XX SV40MEM polypeptide; signal peptide; fibroblast growth factor;  
 KW SV40 large antigen; nuclear localisation signal; NLS;  
 KW immunosuppressive activity; inhibition; nuclear translocation inhibitor;  
 KW kappa immunoglobulin light chain expression; S. typhosa LPS;  
 KW nuclear translocation; treatment; immune disorder; autoimmune disease;  
 KW hypersensitivity; sepsis; prevention; septic shock; antiviral agent;  
 KW tumour growth suppressor; MEM.  
 XX

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:51:16 ; Search time 30.7097 Seconds  
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45.604 Million cell updates/sec

Title: US-10-009-809-3

Perfect score: 70

Sequence: 1 AAVALLPAVLLALLAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Issued patents: AA\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	70	100.0	16	1	US-08-258-852-5
3	70	100.0	16	1	US-08-928-958-4
4	70	100.0	16	1	US-09-072-429-4
5	70	100.0	16	2	US-08-964-302A-3
6	70	100.0	16	2	US-09-170-754B-5
7	70	100.0	16	2	US-09-441-416A-3
8	70	100.0	16	2	US-09-411-706-1
9	70	100.0	16	2	US-09-230-548-19
10	70	100.0	16	2	US-09-450-071A-5
11	70	100.0	16	2	US-09-935-032-1
12	70	100.0	16	2	US-10-083-889-7
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## ALIGNMENTS

RESULT 1  
US-08-642-493-1  
; Sequence 1, Application US/08642493  
; Patent No. 5736394  
; GENERAL INFORMATION:  
; APPLICANT: Coleman, Peter S.  
; APPLICANT: Sheldon, Katherine  
; TITLE OF INVENTION: CELLULAR UPTAKE OF MODIFIED PEPTIDES  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: ME  
; COUNTRY: USA  
; ZIP: 03911  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/642,493  
; FILING DATE:  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M.  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: BBRI-9602  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-642-493-1  
Query Match 100.0%; Score 70; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00023;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 AAVALPAAVLLALLAP 16  
| | | | | | | | | | | | | | | |  
RESULT 2  
US-08-258-852-5  
; Sequence 5, Application US/08258852  
; Patent No. 5807746  
; GENERAL INFORMATION:  
; APPLICANT: Lin, Yao-Zhong  
; APPLICANT: Hawiger, Jack J.  
; TITLE OF INVENTION: A NOVEL METHOD FOR IMPORTING  
; BIOLOGICALLY ACTIVE MOLECULES INTO CELLS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
; STREET: 127 Peachtree Street, N.E.  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303-1811

COMPUTER READABLE FORM:  
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; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/258,852  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perryman, David G.  
; REGISTRATION NUMBER: 33,438  
; REFERENCE/DOCKET NUMBER: 2200.021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404/688-0770  
; TELEFAX: 404/688-9880  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..16  
; OTHER INFORMATION: /label= a  
; OTHER INFORMATION: /note= "Signal peptide of K-PGF"  
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Best Local Similarity 100.0%; Pred. No. 0.00023;  
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Db 1 AAVALPAAVLLALLAP 16  
| | | | | | | | | | | | | | | |  
RESULT 3  
US-08-928-958-4  
; Sequence 4, Application US/08928958  
; Patent No. 5877282  
; GENERAL INFORMATION:  
; APPLICANT: NADLER, STEVEN G.  
; APPLICANT: CLEVELAND, JEFFREY S.  
; APPLICANT: BLAKE, JAMES  
; APPLICANT: HAFKAR, OMAR K.  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN  
; TRANSLLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND  
; METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROBINS & ASSOCIATES  
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
; CITY: MENLO PARK  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/928,958  
; FILING DATE: 12-SRP-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/026978  
; FILING DATE: 20-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ROBINS, ROBERTA L.

GenCore version 5.1.9  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM protein - protein search, using sw model  
 Run on: July 10, 2006, 16:55:10 ; Search time 59.3548 Seconds  
 (without alignments)  
 124.867 Million cell updates/sec

Title: US-10-009-809-3  
 Perfect score: 70  
 Sequence: 1 AAVALLPAVLLALLAP 16

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main:\*

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- 4: /EMC\_Ce1erra\_SID33/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Ce1erra\_SID33/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Ce1erra\_SID33/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	16	3	US-09-214-371-45
2	70	100.0	16	3	US-09-811-870-5
3	70	100.0	16	3	US-09-785-802A-9
4	70	100.0	16	3	US-09-962-967A-3
5	70	100.0	16	3	US-09-965-876A-3
6	70	100.0	16	3	US-09-789-831-12
7	70	100.0	16	4	US-10-226-956-285
8	70	100.0	16	4	US-10-077-555-7
9	70	100.0	16	4	US-10-211-088-303
10	70	100.0	16	4	US-10-136-738-18
11	70	100.0	16	4	US-10-156-570A-26
12	70	100.0	16	4	US-10-144-549-18
13	70	100.0	16	4	US-10-185-593-4
14	70	100.0	16	4	US-10-232-410-1
15	70	100.0	16	4	US-10-261-161-22
16	70	100.0	16	4	US-10-465-826-27
17	70	100.0	16	4	US-10-751-380-7
18	70	100.0	16	4	US-10-688-299-18
19	70	100.0	16	4	US-10-319-316-5
20	70	100.0	16	4	US-10-722-176A-6
21	70	100.0	16	4	US-10-722-176A-9
22	70	100.0	16	5	US-10-148-457A-5
23	70	100.0	16	5	US-10-823-259-37
24	70	100.0	16	5	US-10-823-254-37
25	70	100.0	16	5	US-10-916-185-16
26	70	100.0	16	5	US-10-700-971C-7
27	70	100.0	16	5	US-10-927-262A-45
28	70	100.0	16	5	US-10-319-316-4
29	70	100.0	16	5	US-10-991-286A-46
30	70	100.0	16	5	US-10-899-912A-39
31	70	100.0	16	5	US-10-985-426-16
32	70	100.0	16	5	US-10-909-769-1
33	70	100.0	16	5	US-10-535-780-2
34	70	100.0	16	5	US-10-923-112A-37
35	70	100.0	16	6	US-11-027-967-4
36	70	100.0	16	6	US-11-004-795A-117
37	70	100.0	16	6	US-11-004-379-22
38	70	100.0	16	6	US-11-004-794A-101
39	70	100.0	16	6	US-11-068-717-9
40	70	100.0	16	6	US-11-016-542-6
41	70	100.0	16	6	US-11-078-256-285
42	70	100.0	16	6	US-11-223-699A-4
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49	70	100.0	20	6	US-11-001-674-1
50	70	100.0	20	6	US-11-001-674-2
51	70	100.0	20	6	US-11-223-699A-80
52	70	100.0	20	6	US-11-121-566A-80
53	70	100.0	22	4	US-10-136-738-45
54	70	100.0	22	4	US-10-688-299-45
55	70	100.0	22	6	US-11-223-699A-45
56	70	100.0	22	6	US-11-121-566A-45
57	70	100.0	26	3	US-09-998-350-18
58	70	100.0	26	3	US-09-998-350-19
59	70	100.0	26	3	US-09-997-465B-1
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61	70	100.0	26	4	US-10-201-389A-15
62	70	100.0	26	4	US-10-427-160A-15
63	70	100.0	26	4	US-10-465-826-10
64	70	100.0	26	4	US-10-465-826-11
65	70	100.0	26	4	US-10-465-826-12
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73	70	100.0	26	4	US-10-465-826-23
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83	70	100.0	26	4	US-10-319-316-13
84	70	100.0	26	4	US-10-444-853A-508
85	70	100.0	26	5	US-10-148-457A-1
86	70	100.0	26	5	US-10-148-457A-3
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89	70	100.0	26	5	US-10-148-457A-13
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92	70	100.0	26	5	US-10-826-966-508
93	70	100.0	26	5	US-10-878-175B-45
94	70	100.0	26	5	US-10-923-112A-45
95	70	100.0	26	6	US-11-040-557-3
96	70	100.0	26	6	US-11-111-463-8
97	70	100.0	26	6	US-11-141-725-5
98	70	100.0	26	6	US-11-224-819-18
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## ALIGNMENTS

## RESULT 1

US-09-214-371-45  
; Sequence 45, Application US/09214371B  
; Patent No. US20010018511A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Picklesley, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
; FILE REFERENCES: 4-20937/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/214,371B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-07-04  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 45  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
US-09-214-371-45

Query Match 100.0%; Score 70; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVALLPAVLLALLAP 16  
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DB 1 AAVALLPAVLLALLAP 16

## RESULT 2

US-09-811-870-5  
; Sequence 5, Application US/09811870  
; Publication No. US20020031820A1  
; GENERAL INFORMATION:  
; APPLICANT: Cole, Philip  
; APPLICANT: Parang, Keykavous  
; APPLICANT: Abloogu, Ararat  
; APPLICANT: Kohanski, Ronald  
; APPLICANT: Courtney, Aliya  
; TITLE OF INVENTION: Bisubstrate Inhibitors of Kinases  
; FILE REFERENCES: 001107.00108  
; CURRENT APPLICATION NUMBER: US/09/811,870  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR FILING DATE: 60/190,799  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: kinase substrates  
US-09-811-870-5

Query Match 100.0%; Score 70; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVALLPAVLLALLAP 16  
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DB 1 AAVALLPAVLLALLAP 16

## RESULT 3

US-09-785-802A-9  
; Sequence 9, Application US/09785802A  
; Patent No. US20020151004A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig, Roger  
; TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME  
; FILE REFERENCE: 11067/2035  
; CURRENT APPLICATION NUMBER: US/09/785,802A  
; CURRENT FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: US 09/748,06  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/748,789  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 9  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-785-802A-9

Query Match 100.0%; Score 70; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVALLPAVLLALLAP 16  
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DB 1 AAVALLPAVLLALLAP 16

## RESULT 4

US-09-962-967A-3  
; Sequence 3, Application US/09962967A  
; Publication No. US20030004112A1  
; GENERAL INFORMATION:  
; APPLICANT: Potter, David A.  
; APPLICANT: Skolnik, Paul R.  
; TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF CALPAIN  
; FILE REFERENCE: 00398-140002  
; CURRENT APPLICATION NUMBER: US/09/962,967A  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 09/441,416  
; PRIOR FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: US 08/964,302  
; PRIOR FILING DATE: 1997-11-04  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetically generated peptide  
US-09-962-967A-3

Query Match 100.0%; Score 70; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVALLPAVLLALLAP 16  
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DB 1 AAVALLPAVLLALLAP 16

## RESULT 5

US-09-965-876A-3  
; Sequence 3, Application US/09965876A



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:55:23 ; Search time 4.3871 Seconds  
(without alignments)  
97.858 Million cell updates/sec

Title: US-10-009-809-3

Perfect score: 70

Sequence: 1 AAVALLPAVLALLAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	16	7	US-11-214-588-27
2	70	100.0	16	7	US-11-263-230-296
3	70	100.0	16	7	US-11-259-133-109
4	70	100.0	16	7	US-11-259-266-37
5	70	100.0	16	7	US-11-259-267-37
6	70	100.0	26	7	US-11-214-588-10
7	70	100.0	26	7	US-11-214-588-11
8	70	100.0	26	7	US-11-214-588-12
9	70	100.0	26	7	US-11-214-588-16
10	70	100.0	26	7	US-11-214-588-17
11	70	100.0	26	7	US-11-214-588-18
12	70	100.0	26	7	US-11-214-588-19
13	70	100.0	26	7	US-11-214-588-20
14	70	100.0	26	7	US-11-214-588-21
15	70	100.0	26	7	US-11-214-588-22
16	70	100.0	26	7	US-11-214-588-23
17	70	100.0	26	7	US-11-214-588-24
18	70	100.0	26	7	US-11-214-588-25
19	70	100.0	26	7	US-11-214-588-26
20	70	100.0	26	7	US-11-214-588-29
21	70	100.0	26	7	US-11-214-588-30
22	63	90.0	15	7	US-11-251-734-3
23	63	90.0	26	7	US-11-214-588-9
24	63	90.0	26	7	US-11-214-588-13
25	52	74.3	34	7	US-11-223-610-62

26	64.3	45	64.3	433	6	US-10-718-933-2	Sequence 2, Appli
27	64.3	45	64.3	450	6	US-10-718-933-4	Sequence 4, Appli
28	64.3	45	64.3	457	6	US-10-718-933-20	Sequence 20, Appl
29	62.9	44	62.9	605	6	US-10-449-902-45413	Sequence 45413, A
30	60.0	42	60.0	126	6	US-10-449-902-47965	Sequence 47965, A
31	58.6	41	58.6	447	6	US-10-718-933-5	Sequence 5, Appli
32	57.1	40	57.1	111	6	US-10-449-902-33886	Sequence 33886, A
33	57.1	40	57.1	419	6	US-10-471-571A-2198	Sequence 2198, Ap
34	57.1	40	57.1	876	6	US-10-449-902-42265	Sequence 42265, A
35	55.7	39	55.7	10	7	US-11-223-610-61	Sequence 61, Appl
36	55.7	39	55.7	70	6	US-10-449-902-28743	Sequence 28743, A
37	55.7	39	55.7	206	6	US-10-953-349-17184	Sequence 17184, A
38	55.7	39	55.7	260	6	US-10-953-349-17183	Sequence 17183, A
39	55.7	39	55.7	369	6	US-10-953-349-17182	Sequence 17182, A
40	55.7	39	55.7	396	6	US-10-449-902-50121	Sequence 50121, A
41	55.7	39	55.7	435	6	US-10-449-902-52840	Sequence 52840, A
42	55.7	39	55.7	452	6	US-10-718-933-6	Sequence 6, Appli
43	55.7	39	55.7	479	6	US-10-718-933-7	Sequence 7, Appli
44	55.7	39	55.7	479	6	US-10-718-933-8	Sequence 8, Appli
45	55.7	39	55.7	485	7	US-11-174-307B-3070	Sequence 3070, Ap
46	55.7	39	55.7	493	6	US-10-953-349-34028	Sequence 34028, A
47	54.3	38	54.3	153	6	US-10-953-349-29382	Sequence 29382, A
48	54.3	38	54.3	195	6	US-10-953-349-35922	Sequence 35922, A
49	54.3	38	54.3	200	6	US-10-953-349-35921	Sequence 35921, A
50	54.3	38	54.3	229	6	US-10-953-349-14814	Sequence 14814, A
51	54.3	38	54.3	366	6	US-10-449-902-39380	Sequence 39380, A
52	54.3	38	54.3	392	7	US-11-174-307B-3570	Sequence 3570, Ap
53	54.3	38	54.3	404	6	US-10-471-571A-2804	Sequence 2804, Ap
54	54.3	38	54.3	471	6	US-10-449-902-49263	Sequence 49263, A
55	54.3	38	54.3	508	6	US-10-449-902-44377	Sequence 44377, A
56	54.3	38	54.3	508	6	US-10-449-902-46271	Sequence 46271, A
57	54.3	38	54.3	508	6	US-10-449-902-54149	Sequence 54149, A
58	54.3	38	54.3	581	6	US-10-449-902-41475	Sequence 41475, A
59	53.6	37	53.6	307	6	US-10-449-902-49540	Sequence 49540, A
60	52.9	37	52.9	213	6	US-10-449-902-39389	Sequence 39389, A
61	52.9	37	52.9	242	6	US-10-953-349-29318	Sequence 29318, A
62	52.9	37	52.9	252	6	US-10-953-349-29317	Sequence 29317, A
63	52.9	37	52.9	271	6	US-10-953-349-29316	Sequence 29316, A
64	52.9	37	52.9	297	6	US-10-449-902-48587	Sequence 48587, A
65	52.9	37	52.9	465	6	US-10-449-902-38435	Sequence 38435, A
66	52.9	37	52.9	471	6	US-10-449-902-38281	Sequence 38281, A
67	52.9	37	52.9	512	6	US-10-449-902-44616	Sequence 44616, A
68	52.9	37	52.9	544	7	US-11-251-208-393	Sequence 393, App
69	52.9	37	52.9	758	6	US-10-449-902-41203	Sequence 41203, A
70	52.9	37	52.9	835	6	US-10-449-902-41524	Sequence 41524, A
71	52.9	37	52.9	1060	6	US-10-505-928-729	Sequence 729, App
72	51.4	36	51.4	239	6	US-10-449-902-49145	Sequence 49145, A
73	51.4	36	51.4	294	6	US-10-449-902-43567	Sequence 43567, A
74	51.4	36	51.4	300	6	US-10-953-349-30210	Sequence 30210, A
75	51.4	36	51.4	372	6	US-10-449-902-45749	Sequence 45749, A
76	51.4	36	51.4	416	7	US-11-174-307B-5298	Sequence 5298, Ap
77	51.4	36	51.4	434	6	US-10-953-349-33879	Sequence 33879, A
78	51.4	36	51.4	453	6	US-10-449-902-47037	Sequence 47037, A
79	51.4	36	51.4	459	6	US-10-953-349-33878	Sequence 33878, A
80	51.4	36	51.4	481	7	US-11-197-712-271	Sequence 271, App
81	51.4	36	51.4	507	6	US-10-953-349-33877	Sequence 33877, App
82	51.4	36	51.4	509	6	US-10-449-902-33141	Sequence 33141, A
83	51.4	36	51.4	509	6	US-10-449-902-43057	Sequence 43057, A
84	51.4	36	51.4	509	6	US-10-449-902-43119	Sequence 43119, A
85	51.4	36	51.4	509	6	US-10-449-902-44368	Sequence 44368, A
86	51.4	36	51.4	509	6	US-10-449-902-45701	Sequence 45701, A
87	51.4	36	51.4	509	6	US-10-449-902-56301	Sequence 56301, A
88	51.4	36	51.4	547	6	US-10-449-902-36411	Sequence 36411, A
89	51.4	36	51.4	583	6	US-10-449-902-39694	Sequence 39694, A
90	51.4	36	51.4	583	6	US-10-449-902-54965	Sequence 54965, A
91	51.4	36	51.4	616	6	US-10-196-749-158	Sequence 158, App
92	51.4	36	51.4	2471	7	US-11-071-796A-23	Sequence 23, Appl
93	50.7	35	50.7	552	6	US-10-509-131-50	Sequence 50, Appl
94	50.7	35	50.7	563	6	US-10-509-131-40	Sequence 40, Appl
95	50.0	35	50.0	109	6	US-10-471-571A-4112	Sequence 4112, Ap
96	50.0	35	50.0	113	6	US-10-449-902-42481	Sequence 42481, A
97	50.0	35	50.0	146	6	US-10-449-902-48456	Sequence 48456, A
98	50.0	35	50.0	178	6	US-10-449-902-51347	Sequence 51347, A

99 35 50.0 213 6 US-10-449-902-32810 Sequence 32810, A  
100 35 50.0 213 6 US-10-449-902-43174 Sequence 43174, A

ALIGNMENTS

RESULT 1  
US-11-214-588-27  
; Sequence 27, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 27  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-214-588-27

Query Match 100.0%; Score 70; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVALLPAVLALLAP 16  
Db 1 AAVALLPAVLALLAP 16

RESULT 2  
US-11-263-230-296  
; Sequence 296, Application US/11263230  
; Publication No. US20060115485A1  
; GENERAL INFORMATION:  
; APPLICANT: Losonsky, Genevieve  
; APPLICANT: Connor, Edward M.  
; APPLICANT: Young, James F.  
; APPLICANT: Wu, Herren  
; APPLICANT: Dall'Acqua, William  
; TITLE OF INVENTION: Methods of Preventing and Treating RSV Infections  
; FILE REFERENCE: 10271-174-999  
; CURRENT APPLICATION NUMBER: US/11/263,230  
; CURRENT FILING DATE: 2005-10-31  
; PRIOR APPLICATION NUMBER: 60/623,821  
; PRIOR FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: 60/675,724  
; PRIOR FILING DATE: 2005-04-27  
; PRIOR APPLICATION NUMBER: 60/681,233  
; PRIOR FILING DATE: 2005-05-13  
; PRIOR APPLICATION NUMBER: 60/718,719  
; PRIOR FILING DATE: 2005-09-21  
; PRIOR APPLICATION NUMBER: 60/727,042  
; PRIOR FILING DATE: 2005-10-14  
; PRIOR APPLICATION NUMBER: 60/727,043  
; PRIOR FILING DATE: 2005-10-14  
; NUMBER OF SEQ ID NOS: 1496  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 296  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

; OTHER INFORMATION: intrabody  
US-11-263-230-296

Query Match 100.0%; Score 70; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVALLPAVLALLAP 16  
Db 1 AAVALLPAVLALLAP 16

RESULT 3  
US-11-259-133-109  
; Sequence 109, Application US/11259133  
; Publication No. US20060121042A1  
; GENERAL INFORMATION:  
; APPLICANT: Dall'Acqua, William  
; APPLICANT: Damschroder, Melissa  
; APPLICANT: Kinch, Michael  
; APPLICANT: Carles-Kinch, Kelly  
; TITLE OF INVENTION: MODULATION OF ANTIBODY SPECIFICITY BY TAILORING THE AFFINITY TO  
; FILE REFERENCE: BE700US  
; CURRENT APPLICATION NUMBER: US/11/259,133  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: 60/622,711  
; PRIOR FILING DATE: 2004-10-27  
; PRIOR APPLICATION NUMBER: 60/717,209  
; PRIOR FILING DATE: 2005-09-16  
; NUMBER OF SEQ ID NOS: 205  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 109  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-259-133-109

Query Match 100.0%; Score 70; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVALLPAVLALLAP 16  
Db 1 AAVALLPAVLALLAP 16

RESULT 4  
US-11-259-266-37  
; Sequence 37, Application US/11259266  
; Publication No. US20060121043A1  
; GENERAL INFORMATION:  
; APPLICANT: Kinch, Michael  
; APPLICANT: Carles-Kinch, Kelly  
; TITLE OF INVENTION: Use of Modulators of EphA2 and EphrinA1 for the Treatment and Pre  
; FILE REFERENCE: EP350US  
; CURRENT APPLICATION NUMBER: US/11/259,266  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: 60/622,489  
; PRIOR FILING DATE: 2004-10-27  
; PRIOR APPLICATION NUMBER: 60/705,705  
; PRIOR FILING DATE: 2005-08-03  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 37  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-259-266-37

Query Match 100.0%; Score 70; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:50:59 ; Search time 7.74194 Seconds  
(without alignments)  
198.848 Million cell updates/sec

Title: US-10-009-809-3

Perfect score: 70

Sequence: 1 AAVALLPAVLLALLAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 80.\*

1: piri.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	206	1 TVRHUS	fibroblast growth
2	63	90.0	206	2 JC4268	fibroblast growth
3	49	70.0	194	2 I50710	fibroblast growth
4	47	67.1	317	2 E83344	probable adhesion
5	45	64.3	488	2 S13423	stromelysin 3 (EC
6	44	62.9	74	2 D84231	hypothetical prote
7	43	61.4	120	2 T44554	hypothetical prote
8	43	61.4	334	2 G84123	iron (III) dicitra
9	43	61.4	660	2 E85499	hypothetical prote
10	43	61.4	660	2 E90648	hypothetical prote
11	43	61.4	660	2 A64739	ferrichrome-iron t
12	43	61.4	1094	2 F70697	probable arabinosy
13	43	61.4	1251	2 A57293	latent transformin
14	42	60.0	219	2 AE0945	probable exported
15	42	60.0	256	2 T35133	hypothetical prote
16	42	60.0	447	2 B82490	probable Na+/H+ an
17	42	60.0	878	2 T17245	hypothetical prote
18	41	58.6	193	2 E69675	CDP-diacylglycerol
19	41	58.6	301	2 F86647	hypothetical prote
20	41	58.6	342	2 JC7110	brain-specific mem
21	41	58.6	363	2 G83954	flagella-associate
22	41	58.6	383	2 AF3503	benzoate membrane
23	41	58.6	418	2 E97334	UDP-N-acetylglucos
24	41	58.6	5376	2 T42215	zonadhesin - mouse
25	40	57.1	177	2 AH1232	hypothetical prote
26	40	57.1	244	2 JC8019	CD58 protein - pig
27	40	57.1	261	2 T37948	probable ui small
28	40	57.1	364	2 D95959	conserved hypothet
29	40	57.1	419	2 A99906	hypothetical prote

30	40	57.1	423	2 AH1393	UDP-N-acetylglucos
31	40	57.1	423	2 AC1769	UDP-N-acetylglucos
32	40	57.1	428	2 H84122	UDP-N-acetylglucos
33	40	57.1	429	2 G32354	UDP-N-acetylglucos
34	40	57.1	481	2 B75480	hypothetical prote
35	40	57.1	501	2 H83615	probable MFS trans
36	40	57.1	509	2 G82809	amino acid transpo
37	40	57.1	512	2 E83060	iron (III)-transpo
38	40	57.1	585	2 T51361	nitrate transporte
39	40	57.1	771	2 S18624	ntry protein - Azo
40	40	57.1	858	2 T08881	prominin - mouse
41	39.5	56.4	1002	2 G70876	probable transmemb
42	39	55.7	121	2 B84375	hypothetical prote
43	39	55.7	202	2 D75383	conserved hypothet
44	39	55.7	235	2 AF3403	phosphatidylglycer
45	39	55.7	272	2 H97225	uncharacterized co
46	39	55.7	282	2 D72679	hypothetical prote
47	39	55.7	283	2 S27863	Ts-32K protein - T
48	39	55.7	303	2 D83082	probable permealase
49	39	55.7	308	2 JC7125	epidermal growth f
50	39	55.7	320	2 AH0598	probable membrane
51	39	55.7	323	2 AC3202	hypothetical prote
52	39	55.7	335	2 AD3430	probable undecapre
53	39	55.7	419	2 A95125	hypothetical prote
54	39	55.7	419	2 E97995	UDP-N-acetylglucos
55	39	55.7	425	2 S78258	probable transloca
56	39	55.7	479	2 A55382	nicotinic acetylch
57	39	55.7	491	2 AG0557	AmpG protein limpo
58	39	55.7	491	2 G90689	regulates beta-lac
59	39	55.7	491	2 C85540	signal transducer
60	39	55.7	491	2 S37391	glucose transport
61	39	55.7	509	2 A32101	glucose transport
62	39	55.7	517	2 AC2070	Na+/H+ antiporter
63	39	55.7	737	2 AG2754	two component sens
64	39	55.7	753	2 E97535	nitrogen regulatio
65	39	55.7	788	2 S48191	probable ubiquinol
66	39	55.7	806	2 T35640	probable sensor ki
67	39	55.7	873	1 QR8BVD	VLDR receptor prec
68	39	55.7	1112	2 T30202	probable chitin sy
69	39	55.7	1462	2 T11648	probable mitotic s
70	39	55.7	3341	1 A42996	genome polypeptid
71	38.5	55.0	478	2 C72658	hypothetical prote
72	38	54.3	29	2 T36654	probable small mem
73	38	54.3	82	2 B83740	hypothetical prote
74	38	54.3	199	2 T40079	hypothetical prote
75	38	54.3	206	2 A86609	glycerol-3-P phosph
76	38	54.3	206	2 B72016	CDP-diacylglycerol
77	38	54.3	243	2 T34870	probable membrane
78	38	54.3	275	2 T45530	probable oligopept
79	38	54.3	308	1 S22931	ubiquinol-cytochro
80	38	54.3	380	2 T11335	ubiquinol-cytochro
81	38	54.3	382	2 H64950	flagellar biosynth
82	38	54.3	382	2 B85801	hypothetical prote
83	38	54.3	382	2 F90952	flagellar biosynth
84	38	54.3	383	2 AF0745	flagellar biosynth
85	38	54.3	383	2 A55546	hypothetical prote
86	38	54.3	384	2 D87599	membrane protein l
87	38	54.3	388	2 C95175	conserved hypothet
88	38	54.3	388	2 D98041	membrane protein m
89	38	54.3	397	2 AF3285	DlEB membrane prot
90	38	54.3	404	2 F89859	translocase - Chia
91	38	54.3	416	2 C81324	ubiquinol-cytochro
92	38	54.3	425	2 AH0122	probable drug effl
93	38	54.3	427	2 H72678	hypothetical prote
94	38	54.3	437	2 E87319	conserved hypothet
95	38	54.3	457	2 G72053	translocase - Chia
96	38	54.3	457	2 B86569	translocase (impor
97	38	54.3	460	2 T35916	conserved hypothet
98	38	54.3	462	2 B81613	preprotein translo
99	38	54.3	494	2 AC0133	probable permealase
100	38	54.3	503	2 S44811	F4AB9.2 protein -

## ALIGNMENTS

```
RESULT 1
TVHUHS
fibroblast growth factor 4 - human
N:Alternate names: heparin secretory transforming protein 1; Kaposi sarcoma oncogene; t
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: A28417; A29876; A29649
R:Yoshida, T.; Miyagawa, K.; Odagiri, H.; Sakamoto, H.; Little, P.F.R.; Terada, M.; Sug
Proc. Natl. Acad. Sci. U.S.A. 84, 7305-7309, 1987
A:Title: Genomic sequence of hst, a transforming gene encoding a protein homologous to f
A:Reference number: A28417; MUID:88041096; PMID:2955959
A:Accession: A28417
A:Molecule type: DNA
A:Residues: 1-206 <YOS>
A:Cross-references: UNIPROT:P08620; UNIPARC:UPI0000040662; DDBJ:J02986; NID:g184430; PID
R;Taira, M.; Yoshida, T.; Miyagawa, K.; Sakamoto, H.; Terada, M.; Sugimura, T.
Proc. Natl. Acad. Sci. U.S.A. 84, 2980-2984, 1987
A:Title: cDNA sequence of human transforming gene hst and identification of the coding s
A:Reference number: A29876; MUID:87204251; PMID:2953031
A:Accession: A29876
A:Molecule type: mRNA
A:Residues: 1-206 <TAI>
A:Cross-references: UNIPARC:UPI0000040662; GB:J02986; GB:M16338; NID:g184430; PIDN:AA859
R;Delli Bovi, P.; Curatola, A.M.; Kern, F.G.; Greco, A.; Ittmann, M.; Basillio, C.
Cell 50, 729-737, 1987
A:Title: An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes a growth f
A:Reference number: A29649; MUID:87301716; PMID:2957062
A:Accession: A29649
A:Molecule type: mRNA
A:Residues: 1-206 <BOV>
A:Cross-references: UNIPARC:UPI0000040662; GB:M17446; NID:g186785; PIDN:AAA59473.1; PID:
C:Comment: This protein is an oncogene for Kaposi's sarcoma. It is homologous to the mo
C:Genetics:
A:Gene: GDB:FGF4; HSTF1
A:Cross-references: GDB:120066; OMIM:164980
A:Map position: 11q13.3-11q13.3
A:Introns: 114/1; 148/3
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; Kaposi sarcoma; transforming protein

Query Match 100.0%; Score 70; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVALLPAVLLALLAP 16
Db 7 AAVALLPAVLLALLAP 22

RESULT 2
JC4268
fibroblast growth factor 4 - bovine
N:Alternate names: transforming protein hst
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 17-Mar-2000
C:Accession: JC4268
R;Yu, J.C.; DeSaabra, A.J.J.; Wang, L.M.; Fleming, T.P.; Chedid, M.; Mikl, T.; Heidaran,
Gene 162, 333-334, 1995
A:Title: An unexpected transforming gene in calf-thymus carrier DNA: Bovine hst.
A:Reference number: JC4268; MUID:96032369; PMID:7557455
A:Accession: JC4268
A:Molecule type: mRNA
A:Residues: 1-206 <YUJ>
A:Cross-references: UNIPARC:UPI0000176539; GB:U15969
A:Note: The authors translated the codon GGC for residue 114 as Ser
C:Comment: This protein is a member of fibroblast growth factor family. The hstgene in c
C:Genetics:
A:Gene: hst
A:Introns: 113/3; 145/2
C:Superfamily: fibroblast growth factor
```

C:Keywords: thymus; transforming protein

Query Match 90.0%; Score 63; DB 2; Length 206;  
Best Local Similarity 87.5%; Pred. No. 0.026;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAVALLPAVLLALLAP 16

Db 7 AAVALLPAVLLALLAP 22

## RESULT 3

IS0710

fibroblast growth factor 4 - chicken

C:Species: Gallus gallus (chicken)

C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004

C:Accession: S78506; S50858; I50710

R;Niawander, L.

submitted to the EMBL Data Library, September 1994

A:Reference number: S78506

A:Accession: S78506

A:Molecule type: DNA

A:Residues: 1-194 <NIS>

A:Cross-references: UNIPROT:P49804; UNIPARC:UPI000012A715; EMBL:U14654; NID:g609347; PII

R;Niawander, L.; Jeffery, S.; Martin, G.R.; Tickle, C.

Nature 371, 609-612, 1994

A:Title: A positive feedback loop coordinates growth and patterning in the vertebrate li

A:Reference number: I50710; MUID:95021713; PMID:7935794

A:Accession: S50858

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-136, 'O', 137-194, 'I', <NIW>

A:Cross-references: UNIPARC:UPI000017653A; EMBL:U14654; NID:g609347; PIDN:AAA58706.1; P1

C:Genetics:

A:Gene: FGF4

C:Superfamily: fibroblast growth factor

C:Keywords: growth factor; transforming protein

Query Match 70.0%; Score 49; DB 2; Length 194;

Best Local Similarity 68.8%; Pred. No. 3;

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAVALLPAVLLALLAP 16

Db 3 AAVALLPAVLLALLAP 18

## RESULT 4

ES3344

probable adhesion protein PA2407 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

C:Accession: E83344

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bl

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: E83344

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-317 <STO>

A:Cross-references: UNIPROT:Q91174; UNIPARC:UPI00000C56B6; GB:AE004668; GB:AE004091; N1

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2407

C:Superfamily: adhesin B

Query Match 67.1%; Score 47; DB 2; Length 317;

Best Local Similarity 84.6%; Pred. No. 9.1;

Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:50:27 ; Search time 59.0968 Seconds  
(without alignments)  
250.441 Million cell updates/sec

Title: US-10-009-809-3

Perfect score: 70

Sequence: 1 AAVALLPAVLLALLAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt\_7.2.\*

1: uniprot\_spport.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	206	1 FGF4_HUMAN	P08620 homo sapien
2	63	90.0	206	1 FGF4_BOVIN	P48803 bos taurus
3	57	81.4	329	2 Q3J3B3_RHOS4	Q3J3b3 rhodobacter
4	51	72.9	479	2 Q45R98_STRFR	Q45r98 streptomyc
5	49	70.0	194	1 FGF4_CHICK	P48804 gallus gall
6	49	70.0	206	2 Q9KZV1_STRCO	Q9kzv1 streptomyc
7	48	68.6	249	2 Q3IMB5_NATPD	Q3imb5 natronomona
8	47	67.1	201	2 Q3A0U5_PELCD	Q3aou5 pelobacter
9	47	67.1	285	2 Q72FG9_DESVH	Q72fg9 desulfovibr
10	47	67.1	317	2 Q91174_PSEAE	Q91174 pseudomonas
11	47	67.1	402	2 Q3NYK4_9GAMM	Q3nyk4 shewanella
12	47	67.1	480	2 Q33WH1_9GAMM	Q33wh1 shewanella
13	47	67.1	551	2 Q8W0B2_ORYSA	Q8w0b2 oryza sativ
14	47	67.1	828	1 CAD22_HUMAN	Q9uj99 homo sapien
15	46	65.7	340	2 Q2XB84_PSEPU	Q2xb84 pseudomonas
16	46	65.7	340	2 Q88PY1_PSEPK	Q88py1 pseudomonas
17	46	65.7	431	2 Q2RVB5_RRHOR	Q2rvb5 rhodospirill
18	46	65.7	431	2 Q9AM70_RRHOR	Q9am70 rhodospirill
19	46	65.7	439	2 Q2SLD2_9GAMM	Q2slid2 habella che
20	46	65.7	445	2 Q3QK98_9GAMM	Q3qk98 shewanella
21	46	65.7	799	2 Q34VA2_9GAMM	Q34va2 alkalilimni
22	45	64.3	229	2 Q3V9L4_9SPHN	Q3v9l4 shingopyxi
23	45	64.3	328	2 Q848W5_BACME	Q848w5 bacillus me
24	45	64.3	450	1 ACH10_HUMAN	Q9gzze homo sapien
25	45	64.3	488	1 MMP11_HUMAN	P24347 homo sapien
26	45	64.3	557	2 Q411Z7_KINRA	Q411z7 kineococcus
27	45	64.3	963	2 Q3V9Z0_9SPHN	Q3v9z0 shingopyxi
28	44	62.9	32	2 Q2JT51_9CYAN	Q2jt51 cyanobacter
29	44	62.9	74	2 Q9HRE2_HALSA	Q9hre2 halobacteri
30	44	62.9	124	2 Q6CE02_YARLW	Q6ce02 yarrowia li
31	44	62.9	196	2 Q3J4F9_RHOS4	Q3j4f9 rhodobacter

32	44	62.9	266	2	Q2T8F4_BURTH	Q2t8f4 burkholderi
33	44	62.9	267	2	Q8PIV1_XANAC	Q8piv1 xanthomonas
34	44	62.9	310	2	Q744Y1_MYCPA	Q744y1 mycobacteri
35	44	62.9	324	2	Q2PR07_FUGRU	Q2pr07 fuqu rubrip
36	44	62.9	408	2	Q4NBK9_9M1CC	Q4nbk9 artrobacte
37	44	62.9	441	2	Q3OYH3_DESDG	Q3oyh3 desulfovibr
38	44	62.9	444	2	Q3Q5U7_9GAMM	Q3q5u7 shewanella
39	44	62.9	445	2	Q2ZV10_SHEMU	Q2zv10 shewanella
40	44	62.9	461	2	Q728L6_DESVH	Q728l6 desulfovibr
41	44	62.9	462	2	Q2X738_9GAMM	Q2x738 shewanella
42	44	62.9	552	2	Q2USA2_ASPOR	Q2usa2 aspergillus
43	44	62.9	752	2	Q3RJT5_PARDE	Q3rjt5 paracoccus
44	43.5	62.1	396	2	Q88HZ9_PSEPK	Q88hz9 pseudomonas
45	43	61.4	100	2	Q2KA98_RH1ET	Q2ka98 rhizobium e
46	43	61.4	100	2	Q2R0R4_RH1ME	Q2r0r4 rhizobium e
47	43	61.4	110	2	Q5X2J1_LEGPA	Q5x2j1 legionella
48	43	61.4	120	2	Q9KW33_PSEAE	Q9kw33 pseudomonas
49	43	61.4	120	2	Q9S557_PSEAE	Q9s557 pseudomonas
50	43	61.4	120	2	Q9S565_PSEAE	Q9s565 pseudomonas
51	43	61.4	131	2	Q6H4A5_ORYSA	Q6h4a5 oryza sativ
52	43	61.4	147	2	Q37G16_RHOPA	Q37g16 rhodopseudo
53	43	61.4	161	2	Q3PHJ5_PARDE	Q3phj5 paracoccus
54	43	61.4	231	2	Q33XJ9_9GAMM	Q33xj9 shewanella
55	43	61.4	238	2	Q5Z086_NOCFA	Q5z086 nocardia fa
56	43	61.4	265	2	Q2J990_9ACTO	Q2j990 frankia sp.
57	43	61.4	272	2	Q39YD8_GEOMG	Q39y8d geobacter m
58	43	61.4	275	2	Q88PM4_PSEPK	Q88pm4 pseudomonas
59	43	61.4	287	2	Q5YVG6_NOCFA	Q5yvg6 nocardia fa
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61	43	61.4	293	2	Q3FIG7_9BURK	Q3fig7 burkholderi
62	43	61.4	293	2	Q45BK3_9BURK	Q45bk3 burkholderi
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64	43	61.4	334	2	Q9K6D8_BACHD	Q9k6d8 bacillus ha
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67	43	61.4	417	1	MURA2_CLOPE	Mura2 clostridium
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72	43	61.4	445	2	Q2Z4S0_9GAMM	Q2z4s0 shewanella
73	43	61.4	445	2	Q3SV04_9GAMM	Q3sv04 shewanella
74	43	61.4	445	2	Q368E6_9GAMM	Q368e6 shewanella
75	43	61.4	449	2	Q3P3U7_9GAMM	Q3p3u7 shewanella
76	43	61.4	451	2	Q6LNC2_PHOPR	Q6lnc2 photobacter
77	43	61.4	471	2	Q5EMD5_BURPS	Q5emd5 burkholderi
78	43	61.4	471	2	Q3S63_BURP1	Q3s63 burkholderi
79	43	61.4	471	2	Q63UE0_BURPS	Q63ue0 burkholderi
80	43	61.4	472	2	Q9L3C3_ARYMD	Q9l3c3 amycolatops
81	43	61.4	476	2	Q93ME9_ARYMD	Q93me9 amycolatops
82	43	61.4	535	2	Q6MEDI_PARUM	Q6med1 parachlamyd
83	43	61.4	544	2	Q4JWC3_CORJK	Q4jwc3 corynebacte
84	43	61.4	549	2	Q33VW8_RRHOR	Q33vw8 rhodococcus
85	43	61.4	563	2	Q40GD7_RRHOB	Q40gd7 jannaschia
86	43	61.4	660	1	PHUB_ECOLI	PHUB escherichia
87	43	61.4	660	2	Q325Y6_SHIBS	Q325y6 shigella bo
88	43	61.4	660	2	Q32JV5_SHIDS	Q32jv5 shigella dy
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90	43	61.4	660	2	Q8X8Z5_ECO57	Q8x8z5 escherichia
91	43	61.4	660	2	Q83SL5_SHIFL	Q83sl5 shigella fl
92	43	61.4	665	2	Q21FR0_9DELT	Q21fro anaeromyxob
93	43	61.4	760	2	Q2RTR6_RRHOR	Q2rtr6 rhodospirill
94	43	61.4	784	2	Q35EP6_9BRAD	Q35ep6 bradyrhizob
95	43	61.4	804	2	Q3QWU7_9RHOB	Q3qw7 silicibacte
96	43	61.4	1094	1	EMBA_MYCBO	EMBA mycobacteri
97	43	61.4	1094	1	EMBA_MYCTU	P04561 mycobacteri
98	43	60.7	451	2	Q4DD48_TRYCR	Q4dd48 trypanosoma
99	42.5	60.0	90	2	Q8XX11_RALSO	Q8xx11 ralstonia s
100	42	60.0	97	2	Q4W8Y1_ASPFU	Q4w8y1 aspergillus

ALIGNMENTS

```
RESULT 1
FGF4 HUMAN STANDARD; PRT; 206 AA.
AC P08620;
DT 01-AUG-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1988, sequence version 1.
DT 07-FEB-2006, entry version 60.
DE Fibroblast growth factor 4 precursor (FGF-4) (Heparin secretory
DE transforming protein) (HST-1) (HST) (transforming protein KS3) (HBGF-
DE 4).
GN Name=FGF4; Synonyms=HST, HSTF1, KS3;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88041096; PubMed=2959959;
RA Yoshida T., Miyagawa K., Odagiri H., Sakamoto H., Little P.F.R.,
RA Terada M., Sugimura T.;
RT "Genomic sequence of hst, a transforming gene encoding a protein
RT homologous to fibroblast growth factors and the int-2-encoded
RT protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7305-7309(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87204251; PubMed=2953031;
RA Taira M., Yoshida T., Miyagawa K., Sakamoto H., Terada M.,
RA Sugimura T.;
RT "cDNA sequence of human transforming gene hst and identification of
RT the coding sequence required for transforming activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2980-2984(1987).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87301716; PubMed=2957062; DOI=10.1016/0092-8674(87)90331-X;
RA Delli Bovi P., Curatola A.M., Kern F.G., Graco A., Ittmann M.,
RA Basiglio C.;
RT "An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes
RT a growth factor that is a member of the FGF family.";
RL Cell 50:729-737(1987).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 79-206.
RX MEDLINE=21378624; PubMed=11486033;
RX DOI=10.1126/SCIENCE.21.17.5946-5957.2001;
RA Bellosta P., Iwahori A., Plotnikov A.N., Eliseenkova A.V.,
RA Basiglio C., Mohammadi M.;
RT "Identification of receptor and heparin binding sites in fibroblast
RT growth factor 4 by structure-based mutagenesis.";
RL Mol. Cell. Biol. 21:5946-5957(2001).
CC -!- FUNCTION: Can transform NIH 3T3 cells from a human stomach tumor
CC (hst) and from Kaposi's sarcoma (KS3). It has a mitogenic
CC activity.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC -----
DR EMBL: J02986; AA059555.1; -; Genomic_DNA.
DR EMBL: M17446; AA59473.1; -; mRNA.
DR PIR: A28417; TVHUS.
DR FDB: I1J1T; X-ray; A=79-206.
DR Ensembl: ENSG00000075388; Homo sapiens.
DR HGNC: HGNC:3682; FGF4.
DR MIM: 164980; gene.
DR GO: GO:0005576; C:extracellular region; TAS.
DR GO: GO:0008083; F:growth factor activity; TAS.
DR GO: GO:0007267; F:cell-cell signaling; TAS.
DR GO: GO:0008284; F:positive regulation of cell proliferation; TAS.
DR GO: GO:0007165; F:signal transduction; TAS.
DR InterPro: IPR002209; GF heparin_bd.
DR InterPro: IPR002348; ILI_HBGF.
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DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00263; HBGFPGF.
DR PRINTS: PR00262; ILIHBGF.
DR PRODOM: PD000831; ILI_HBGF; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; 1.
KW 3D-structure; Growth factor; Heparin-binding; Mitogen; Proto-oncogene;
KW Signal.
FT SIGNAL. 1 30 Potential.
FT CHAIN 31 206 Fibroblast growth factor 4.
FT /FTID=PRO_0000008953.
FT STRAND 82 88
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Query Match 100.0%; Score 70; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVALLPAVLALLAP 16  
| | | | | | | | | | | | | | | |  
Db 7 AAVALLPAVLALLAP 22

RESULT 2  
FGF4\_BOVIN STANDARD; PRT; 206 AA.  
AC P48803;  
DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.  
DT 01-FEB-1996, sequence version 1.  
DT 07-FEB-2006, entry version 38.  
DE Fibroblast growth factor 4 precursor (FGF-4) (Heparin secretory  
DE transforming protein) (HST) (HBGF-4).  
GN Name=FGF4; Synonyms=HST;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC TISSUE=Thymus.  
RX MEDLINE=96032369; PubMed=7557455; DOI=10.1016/0378-1119(95)00330-9;  
RA Yu J.C., Deseabra A.J., Wang L.M., Fleming T.P., Chedid M., Miki T.,  
RA Heidaran M.A.;  
RT "An unexpected transforming gene in calf-thymus carrier DNA: bovine

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 10, 2006, 16:50:22 ; Search time 105.677 Seconds  
(without alignments)  
112.490 Million cell updates/sec

Title: US-10-009-809-7

Perfect score: 127

Sequence: 1 AAVALLPAVLLALLAPKNLKECGLY 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A\_Geneseq\_8:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

9: Geneseqp2005s:\*

10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127	100.0	26	4	AAY72151 Succinyl
2	127	100.0	26	4	AAY72153 Anti-alle
3	127	100.0	26	4	AAY72139 Anti-alle
4	127	100.0	26	5	AAE26158 Galphai3
5	127	100.0	26	5	AAE26154 Peptide 2
6	127	100.0	26	5	AAE26156 Peptide 2
7	127	100.0	27	4	AAY72146 Anti-alle
8	127	100.0	27	4	AAY72150 N-termina
9	122	96.1	26	5	AAE26141 Galphai3
10	121	95.3	26	5	AAE26142 Galphai3
11	121	95.3	26	5	AAE26145 Galphai3
12	121	95.3	26	5	AAE26137 Galphai3
13	120	94.5	26	4	AAY72144 Modified
14	120	94.5	26	5	AAE26144 Galphai3
15	120	94.5	26	5	AAE26148 Galphai3
16	120	94.5	27	4	AAY72145 Anti-alle
17	119	93.7	26	5	AAE26147 Galphai3
18	119	93.7	26	5	AAE26143 Galphai3
19	118	92.9	26	5	AAE26139 Galphai3
20	117	92.1	26	4	AAY72149 Anti-alle
21	117	92.1	26	5	AAE26138 Galphai3
22	117	92.1	26	5	AAE26146 Galphai3
23	114	89.8	26	4	AAY72152 Succinyl

Aay72142	Anti-alle	24	114	89.8	26	4	AAY72142
Aae26155	Peptide 5	25	114	89.8	26	5	AAE26155
Aay72147	Anti-alle	26	98.5	77.6	23	4	AAY72147
Aay72148	Anti-alle	27	91.5	72.0	23	4	AAY72148
Aaw56391	SV40MEM p	28	85	66.9	30	2	AAW56391
Aay55812	SV40MEM p	29	85	66.9	30	3	AAW55812
Aaw53778	PKR pepti	30	80	63.0	25	2	AAW53778
Aaw53770	PKR pepti	31	79	62.2	22	3	AAW53770
Aaw53770	PKR pepti	32	79	62.2	37	2	AAW53770
Aaw56414	Nuclear t	33	78	61.4	29	2	AAW56414
Aay55835	SV40MEM p	34	78	61.4	29	3	AAW55835
Abu69594	Human NF-	35	78	61.4	29	6	ABU69594
Adub3161	Human NFK	36	78	61.4	29	9	ADUB3161
Adw14501	Peptide u	37	78	61.4	29	9	ADW14501
Adz68077	MAP Kinase	38	77	60.6	26	9	ADZ68077
Adj62657	Rank-asso	39	75.5	59.4	34	8	ADJ62657
Aay67960	Karposi s	40	75	59.1	17	3	AAW67960
Aay67955	Karposi s	41	75	59.1	19	3	AAW67955
Aay67962	Karposi s	42	75	59.1	20	3	AAW67962
Aay67958	Karposi s	43	75	59.1	22	3	AAW67958
Adj62658	Rank-asso	44	75	59.1	34	8	ADJ62658
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Aau03158	Peptide S	46	74	58.3	26	4	AU03158
Adq91933	Kaposi fi	47	74	58.3	26	8	ADQ91933
Aeb48524	Kaposi fi	48	74	58.3	26	9	AEB48524
Aee05504	Kaposi fi	49	74	58.3	26	9	AEE05504
Aee92091	Polynucle	50	74	58.3	28	10	AEE92091
Aee91996	Polynucle	51	74	58.3	28	10	AEE91996
Aee91998	Polynucle	52	74	58.3	28	10	AEE91998
Aee92067	Polynucle	53	74	58.3	28	10	AEE92067
Aee95360	Human/HIV	54	74	58.3	28	10	AEE95360
Aef21077	Human and	55	74	58.3	28	10	AEF21077
Aee91997	Polynucle	56	74	58.3	29	10	AEE91997
Aee92058	Polynucle	57	74	58.3	29	10	AEE92058
Aaw53779	PKR pepti	58	73	57.5	24	2	AAW53779
Aee92006	Polynucle	59	72	56.7	22	10	AEE92006
Aee92080	Polynucle	60	72	56.7	22	10	AEE92080
Aea47616	Amino aci	61	72	56.7	32	9	AEA47616
Aea47608	Amino aci	62	72	56.7	32	9	AEA47608
Aea47617	Amino aci	63	72	56.7	32	9	AEA47617
Aea47614	Amino aci	64	72	56.7	32	9	AEA47614
Aae34469	L-T6Pp-1	65	72	56.7	34	6	AAE34469
Aay89434	Core poly	66	72	56.7	36	3	AAW89434
Aab77835	Core poly	67	72	56.7	36	4	AAB77835
Abb02317	Viral cor	68	72	56.7	36	4	ABB02317
Abb00842	Viral DPI	69	72	56.7	36	4	ABB00842
Aau13388	DPI78-11k	70	72	56.7	36	4	AU13388
Aay13502	Calpastat	71	72	56.7	36	5	ADE02337
Aae15611	kFGF sign	72	71	55.9	40	5	AAE15611
Abu10001	Calpain i	73	71	55.9	40	5	ABU10001
Abu10002	Calpain i	74	71	55.9	40	6	ABU10002
Aar87636	Membrane	75	71	55.9	41	2	AAR87636
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Aau03155	Polypepti	78	71	55.9	41	4	AU03155
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Abu10000	Calpain i	81	71	55.9	41	6	ABU10000
Aar87629	Signal pe	82	71	55.9	41	6	AAR87629
Aaw37753	Chimeric	83	70	55.1	16	2	AAW37753
Aaw56394	MEM poly	84	70	55.1	16	2	AAW56394
Aaw48689	Signal pe	85	70	55.1	16	2	AAW48689
Aaw53769	PKR pepti	86	70	55.1	16	2	AAW53769
Aay13506	Signal se	87	70	55.1	16	2	AAW13506
Aay67954	Karposi s	88	70	55.1	16	3	AAW67954
Aay55815	Fibroblas	89	70	55.1	16	3	AAW55815
Aae02979	Hydrophob	90	70	55.1	16	4	AAE02979
Aau97005	CCAAT enh	91	70	55.1	16	4	AU97005
Aae11949	Membrane	92	70	55.1	16	4	AAE11949
Aau03154	Peptide K	93	70	55.1	16	4	AU03154

97 70 55.1 16 4 AAY72476 Kaposi fi  
 98 70 55.1 16 5 ABG78989 Cell pene  
 99 70 55.1 16 5 AAU10399 Membrane  
 100 70 55.1 16 5 AAEL5613 Kaposi's

## ALIGNMENTS

RESULT 1  
 AAY72151  
 ID AAY72151 standard; peptide; 26 AA.  
 XX  
 AC AAY72151;  
 XX  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Succinylated anti-allergic peptide 2.  
 XX  
 KW Anti-allergic peptide; therapeutic; migraine; psoriasis; asthma;  
 KW multiple sclerosis; nasal allergy; mast cell degranulation; histamine;  
 KW allergy; eye; skin; acute urticaria; interstitial cystitis; vasotropic;  
 KW psychogenic; bowel disease; dermatological; antiinflammatory; G alpha13;  
 KW neuroprotective; antipsoriatic; Kaposi fibroblast growth factor;  
 KW fusion peptide; exocytosis.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..16  
 FT /label= Signal\_peptide  
 FT /note= "Signal sequence of Kaposi fibroblast growth  
 FT factor; this region is referred in claim 48"  
 FT Modified-site 1  
 FT /note= "Succinylated alanine"  
 FT Peptide 17..26  
 FT /label= G\_alpha13\_peptide  
 FT /note= "Corresponds to C-terminal sequence of G alpha13"  
 XX  
 PN WO200078346-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-IL000346.  
 XX  
 PR 17-JUN-1999; 99IL-00130526.  
 XX  
 PA (ALLE-) ALLERGENE LTD.  
 XX  
 PI Eisenberg R, Raz T;  
 XX  
 DR WPI; 2001-080758/09.  
 XX  
 PT Novel anti-allergic agents for treating allergic conditions such as  
 PT allergic reactions in eye, skin, nasal allergy, asthma, migraines, has  
 PT peptides for cell penetration and reducing mast cell degranulation.  
 XX  
 PS Claim 29; Page 44; 63pp; English.  
 XX  
 CC The present sequence is succinylated anti-allergic peptide 2 consisting  
 CC of a signal sequence of Kaposi fibroblast growth factor, linked to the C-  
 CC terminal G alpha13 sequence. This C-terminal G alpha13 appears to mediate  
 CC the peptidergic pathway leading to exocytosis in mast cells. A succinyl  
 CC residue is added to the N-terminus of peptide 2 (AAY72139), for improving  
 CC the peptide solubility. The invention relates to therapeutic complex  
 CC molecules which are useful as anti-allergic agents. These anti-allergic  
 CC agents are useful for treating allergic conditions such as nasal allergy,  
 CC allergic reaction in the eye or skin, acute urticaria, psoriasis,  
 CC psychogenic or allergic asthma, interstitial cystitis, bowel diseases,  
 CC migraines and multiple sclerosis. The therapeutic complex is highly  
 CC specific, direct and provides targeted treatment of allergies and  
 CC related inflammatory conditions. It comprises molecules having at least a  
 CC first segment ie., a signal peptide which is competent for the

CC importation of the complex into the mast cells, and a second segment  
 CC which is having the anti-allergic effect is able to block or  
 CC significantly reduce the G protein-mediated contribution to mast cell  
 CC degranulation and in turn the release of histamine. The invention also  
 CC discloses methods for preventing and treating allergies  
 XX  
 SQ Sequence 26 AA;  
 Query Match 100.0%; Score 127; DB 4; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 3e-12;  
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 Db 1 AAVALLPAVLLALLAPKNNLKECGLY 26  
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 ID AAY72153 standard; peptide; 26 AA.  
 XX  
 AC AAY72153;  
 XX  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Anti-allergic cyclic peptide 2.  
 XX  
 KW Anti-allergic peptide; therapeutic; migraine; psoriasis; asthma;  
 KW multiple sclerosis; nasal allergy; mast cell degranulation; histamine;  
 KW allergy; eye; skin; acute urticaria; interstitial cystitis; vasotropic;  
 KW psychogenic; bowel disease; dermatological; antiinflammatory; G alpha13;  
 KW neuroprotective; antipsoriatic; Kaposi fibroblast growth factor; cyclic;  
 KW fusion peptide; exocytosis.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..16  
 FT /label= Signal\_peptide  
 FT /note= "Signal sequence of Kaposi fibroblast growth  
 FT factor; this region is referred in claim 48"  
 FT Peptide 17..26  
 FT /label= G\_alpha13\_peptide  
 FT /note= "Corresponds to C-terminal sequence of G alpha13"  
 FT Modified-site 17  
 FT /note= "The side chain of Lys residue forms a cyclic bond  
 FT with Tyr found at the C-terminal end"  
 FT Modified-site 26  
 FT /note= "The C-terminal end of the peptide forms a cyclic  
 FT bond with side chain of Lys at position 17"  
 XX  
 PN WO200078346-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-IL000346.  
 XX  
 PR 17-JUN-1999; 99IL-00130526.  
 XX  
 PA (ALLE-) ALLERGENE LTD.  
 XX  
 PI Eisenberg R, Raz T;  
 XX  
 DR WPI; 2001-080758/09.  
 XX  
 PT Novel anti-allergic agents for treating allergic conditions such as  
 PT allergic reactions in eye, skin, nasal allergy, asthma, migraines, has  
 PT peptides for cell penetration and reducing mast cell degranulation.  
 XX  
 PS Example 3; Page 24; 63pp; English.  
 XX  
 CC The present sequence is cyclic anti-allergic peptide 2 consisting of a  
 CC signal sequence of Kaposi fibroblast growth factor, linked to the C-



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:51:16 ; Search time 49.9032 Seconds  
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Title: US-10-009-809-7

Perfect score: 127

Sequence: 1 AAVALLPAVLLALLAPKNLKECGLY 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents\_AA\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	80	63.0	25	2 US-09-230-548-20
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5	78	61.4	29	1 US-08-928-958-24
6	78	61.4	29	1 US-09-072-429-24
7	74	58.3	26	1 US-08-258-852-9
8	74	58.3	26	2 US-09-170-754B-9
9	74	58.3	26	2 US-09-450-071A-9
10	74	58.3	26	5 PCT-US95-07539-9
11	74	58.3	26	5 PCT-US95-07539-9
12	73	57.5	24	2 US-09-230-548-21
13	72	56.7	34	2 US-10-143-293-19
14	72	56.7	36	2 US-09-082-279B-844
15	72	56.7	36	2 US-09-315-304B-844
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17	72	56.7	36	2 US-09-515-965A-844
18	72	56.7	36	2 US-09-350-641C-844
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35	70	55.1	16	1 US-08-258-852-5	Sequence 5, Appli
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45	70	55.1	16	2 US-10-083-889-7	Sequence 7, Appli
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76	70	55.1	30	2 US-09-083-279B-843	Sequence 843, App
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; ALIGNMENTS
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US-08-928-958-1
; Sequence 1, Application US/08928958
; Patent No. 5877282
; GENERAL INFORMATION:
; APPLICANT: NADLER, STEVEN G.
; APPLICANT: CLEVELAND, JEFFREY S.
; APPLICANT: BLAKE, JAMES
; APPLICANT: HAFPAR, OMAR K.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
; TITLE OF INVENTION: TRANSLLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,958
; FILING DATE: 12-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 60/026978
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5998-0019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-928-958-1
Query Match 66.9%; Score 85; DB 1; Length 30;
Best Local Similarity 82.6%; Pred. No. 1.8e-06;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AAVALLPAVLLALLAPKNNLKEC 23
Db 8 AAVALLPAVLLALLAPKNNLKEC 30

RESULT 2
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; Sequence 1, Application US/09072429
; Patent No. 5962415
; GENERAL INFORMATION:
; APPLICANT: Nadler, Steven G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE
; TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLLOCATION AND AN
; TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 24
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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,429
; FILING DATE: 04-MAY-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Klein, Christopher A.
; REGISTRATION NUMBER: 34,363
; REFERENCE/DOCKET NUMBER: ON0141b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 252-3714
; TELEFAX: (609) 252-4526
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-072-429-1
Query Match 66.9%; Score 85; DB 1; Length 30;
Best Local Similarity 82.6%; Pred. No. 1.8e-06;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 8 AAVALLPAVLLALLAPKNNLKEC 30

RESULT 3
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; Sequence 20, Application US/09230548
; Patent No. 6326466
; GENERAL INFORMATION:
; APPLICANT: Bottaro, Donald P.
; APPLICANT: Petryshyn, Raymond
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary,
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Double-Stranded RNA Dependent Protein Kinase Derived
; TITLE OF INVENTION: Peptides to Promote Proliferation of Cells and Tissues
; TITLE OF INVENTION: in a Controlled Manner
; FILE REFERENCE: 015280-286200US
; CURRENT APPLICATION NUMBER: US/09/230,548
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 60/023,307
; EARLIER FILING DATE: 1996-07-30
; EARLIER APPLICATION NUMBER: WO PCT/US97/14350
; EARLIER FILING DATE: 1997-07-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:double-stranded
; OTHER INFORMATION: RNA dependent protein kinase (PKR) peptide
; OTHER INFORMATION: antagonist, cell-membrane permeable peptide
US-09-230-548-20
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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:55:10 ; Search time 96.4516 Seconds  
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124.867 Million cell updates/sec

Title: US-10-009-809-7

Perfect score: 127

Sequence: 1 AAVALLPAVLLALLAPKNNLKECGLY 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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14	117	92.1	26	4	US-10-465-826-12
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25	74	58.3	26	5	US-10-148-457A-9
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69	70	55.1	16	4	US-10-722-176A-9	Sequence 9, Appli
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72	70	55.1	16	5	US-10-823-254-37	Sequence 37, Appli
73	70	55.1	16	5	US-10-916-185-16	Sequence 16, Appli
74	70	55.1	16	5	US-10-700-971C-7	Sequence 7, Appli
75	70	55.1	16	5	US-10-927-262A-45	Sequence 45, Appli
76	70	55.1	16	5	US-10-878-175B-37	Sequence 37, Appli
77	70	55.1	16	5	US-10-991-286A-46	Sequence 46, Appli
78	70	55.1	16	5	US-10-899-912A-39	Sequence 39, Appli
79	70	55.1	16	5	US-10-985-436-16	Sequence 16, Appli
80	70	55.1	16	5	US-10-909-789-1	Sequence 1, Appli
81	70	55.1	16	5	US-10-535-780-2	Sequence 2, Appli
82	70	55.1	16	5	US-10-923-112A-37	Sequence 37, Appli
83	70	55.1	16	6	US-11-027-967-4	Sequence 4, Appli
84	70	55.1	16	6	US-11-004-795A-117	Sequence 117, App
85	70	55.1	16	6	US-11-004-379-22	Sequence 22, Appli
86	70	55.1	16	6	US-11-004-794A-101	Sequence 101, App
87	70	55.1	16	6	US-11-068-717-9	Sequence 9, Appli
88	70	55.1	16	6	US-11-016-542-6	Sequence 6, Appli
89	70	55.1	16	6	US-11-078-256-285	Sequence 285, App
90	70	55.1	16	6	US-11-223-699A-4	Sequence 4, Appli
91	70	55.1	16	6	US-11-121-566A-4	Sequence 4, Appli
92	70	55.1	16	6	US-11-200-703-16	Sequence 16, Appli
93	70	55.1	20	3	US-09-777-560-1	Sequence 1, Appli
94	70	55.1	20	3	US-09-777-560-2	Sequence 2, Appli
95	70	55.1	20	6	US-11-066-697-1058	Sequence 1058, Ap
96	70	55.1	20	6	US-11-066-697-1060	Sequence 1060, Ap
97	70	55.1	20	6	US-11-001-674-1	Sequence 1, Appli
98	70	55.1	20	6	US-11-001-674-2	Sequence 2, Appli
99	70	55.1	20	6	US-11-223-699A-80	Sequence 80, Appli
100	70	55.1	20	6	US-11-121-566A-80	Sequence 80, Appli

## ALIGNMENTS

## RESULT 1

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US-10-465-826-23
; Sequence 23, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamir
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-465-826-23

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## RESULT 2

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US-10-465-826-24
; Sequence 24, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamar
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 26
; TYPE: PRP
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: BINDING
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal amino acid is succin
US-10-465-826-24

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### RESULT 3

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US-10-465-826-26
; Sequence 26, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamir
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465, 826
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (17)..(26)
; OTHER INFORMATION: A bond exists between the side
; OTHER INFORMATION: c
; OTHER INFORMATION: -terminus of the peptide
US-10-465-826-26

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## RESULT 4

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US-10-465-826-29
; Sequence 29, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamir
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PC7/ILO1/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
;
US-10-465-826-29

Query Match 100.0%; Score 127; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.1e-12;
Matches 26; Conservative 0; Mismatches 0;

Qy 1 AAVALLPALLALLAPNNLKCCGLY 26
Db 1 AAVALLPALLALLAPNNLKCCGLY 26

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:55:23 ; Search time 7.12903 Seconds  
(without alignments)  
97.858 Million cell updates/sec

Title: US-10-009-809-7

Perfect score: 127

Sequence: 1 AAVALLPAVLLALLAPKNLKECGLY 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US07\_NEW\_PUB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US08\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US10\_NEW\_PUB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US11\_NEW\_PUB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	127	100.0	26	7	US-11-214-588-24
3	127	100.0	26	7	US-11-214-588-26
4	127	100.0	26	7	US-11-214-588-29
5	123	96.9	26	7	US-11-214-588-10
6	123	96.9	26	7	US-11-214-588-19
7	122	96.1	26	7	US-11-214-588-16
8	121	95.3	26	7	US-11-214-588-11
9	121	95.3	26	7	US-11-214-588-17
10	121	95.3	26	7	US-11-214-588-20
11	119	93.7	26	7	US-11-214-588-9
12	119	93.7	26	7	US-11-214-588-18
13	118	92.9	26	7	US-11-214-588-13
14	117	92.1	26	7	US-11-214-588-12
15	117	92.1	26	7	US-11-214-588-21
16	117	92.1	26	7	US-11-214-588-30
17	114	89.8	26	7	US-11-214-588-25
18	70	55.1	16	7	US-11-214-588-27
19	70	55.1	16	7	US-11-214-588-230-296
20	70	55.1	16	7	US-11-259-133-109
21	70	55.1	16	7	US-11-259-266-37
22	70	55.1	16	7	US-11-259-267-37
23	70	55.1	26	7	US-11-214-588-22
24	65	51.2	26	7	US-11-214-588-15
25	63	49.6	15	7	US-11-251-734-3

26	57	44.9	10	7	US-11-214-588-1	Sequence 1, Appli
27	57	44.9	10	7	US-11-214-588-3	Sequence 3, Appli
28	57	44.9	25	7	US-11-214-588-14	Sequence 14, Appli
29	54	42.5	34	7	US-11-223-610-62	Sequence 62, Appli
30	53	41.7	10	7	US-11-214-588-4	Sequence 4, Appli
31	52	40.9	10	7	US-11-214-588-6	Sequence 6, Appli
32	51	40.2	10	7	US-11-214-588-5	Sequence 5, Appli
33	51	40.2	10	7	US-11-214-588-8	Sequence 8, Appli
34	50	39.4	10	7	US-11-214-588-31	Sequence 31, Appli
35	50	39.4	339	7	US-11-293-697-3642	Sequence 3642, Ap
36	50	39.4	339	7	US-11-293-697-3821	Sequence 3821, Ap
37	49	38.6	333	6	US-10-953-349-28481	Sequence 28481, A
38	49	38.6	337	6	US-10-953-349-28480	Sequence 28480, A
39	49	38.6	345	6	US-10-953-349-28479	Sequence 28479, A
40	47	37.0	10	7	US-11-214-588-7	Sequence 7, Appli
41	47	37.0	10	7	US-11-214-588-32	Sequence 32, Appli
42	47	37.0	273	6	US-10-953-349-9996	Sequence 9996, Ap
43	47	37.0	313	6	US-10-953-349-9995	Sequence 9995, Ap
44	47	37.0	363	6	US-10-953-349-9994	Sequence 9994, Ap
45	47	37.0	591	6	US-10-449-902-46347	Sequence 46347, A
46	45.5	35.8	586	6	US-10-449-902-54318	Sequence 54318, A
47	45	35.4	177	6	US-10-953-349-23008	Sequence 23008, A
48	45	35.4	427	6	US-10-449-902-36344	Sequence 36344, A
49	45	35.4	433	6	US-10-718-933-2	Sequence 2, Appli
50	45	35.4	450	6	US-10-718-933-4	Sequence 4, Appli
51	45	35.4	457	6	US-10-449-902-56379	Sequence 56379, A
52	44.5	35.0	364	6	US-10-449-902-56379	Sequence 2, Appli
53	44	34.6	10	7	US-11-214-588-2	Sequence 18624, A
54	44	34.6	161	6	US-10-953-349-18624	Sequence 18624, A
55	44	34.6	178	6	US-10-449-902-46105	Sequence 46105, A
56	44	34.6	259	6	US-10-471-571A-1160	Sequence 1160, Ap
57	44	34.6	278	6	US-10-953-349-18623	Sequence 18623, A
58	44	34.6	287	6	US-10-953-349-18622	Sequence 18622, A
59	44	34.6	605	6	US-10-449-902-45413	Sequence 45413, A
60	43.5	34.3	305	6	US-10-449-902-31938	Sequence 31938, A
61	43	33.9	127	6	US-10-449-902-42514	Sequence 42514, A
62	43	33.9	127	6	US-10-449-902-45033	Sequence 45033, A
63	43	33.9	422	6	US-10-449-902-53735	Sequence 53735, A
64	42	33.1	126	6	US-10-449-902-47965	Sequence 47965, A
65	42	33.1	402	6	US-10-471-571A-5294	Sequence 5294, Ap
66	42	33.1	431	6	US-10-449-902-29670	Sequence 29670, Ap
67	42	33.1	431	6	US-10-449-902-46587	Sequence 46587, A
68	42	33.1	493	6	US-10-953-349-34028	Sequence 34028, A
69	42	33.1	690	6	US-10-449-902-53535	Sequence 53535, A
70	42	33.1	708	7	US-11-258-767-28	Sequence 28, Appli
71	42	33.1	708	7	US-11-258-767-32	Sequence 32, Appli
72	42	33.1	758	6	US-10-449-902-41203	Sequence 41203, A
73	42	33.1	1220	7	US-11-273-537-34	Sequence 34, Appli
74	41	32.3	387	7	US-11-174-307B-76	Sequence 76, Appli
75	41	32.3	447	6	US-10-718-933-5	Sequence 5, Appli
76	41	32.3	485	6	US-10-471-571A-4490	Sequence 4490, Ap
77	41	32.3	578	6	US-10-449-902-43264	Sequence 43264, A
78	41	32.3	578	6	US-10-449-902-46835	Sequence 46835, A
79	41	32.3	814	6	US-10-449-902-55972	Sequence 55972, A
80	41	32.3	1020	6	US-10-449-902-43322	Sequence 43322, A
81	41	32.3	1020	6	US-10-449-902-46407	Sequence 46407, A
82	41	32.3	1206	6	US-10-449-902-43305	Sequence 43305, A
83	40.5	31.9	415	6	US-10-449-902-49637	Sequence 49637, A
84	40.5	31.9	573	6	US-10-449-902-48458	Sequence 48458, A
85	40	31.5	72	6	US-10-449-902-40858	Sequence 40858, A
86	40	31.5	111	6	US-10-449-902-33886	Sequence 33886, A
87	40	31.5	227	6	US-10-449-902-50398	Sequence 50398, A
88	40	31.5	385	6	US-10-449-902-50398	Sequence 50398, A
89	40	31.5	385	6	US-10-449-902-51110	Sequence 51110, A
90	40	31.5	404	6	US-10-471-571A-2804	Sequence 2804, Ap
91	40	31.5	419	6	US-10-471-571A-2198	Sequence 2198, Ap
92	40	31.5	432	6	US-10-449-902-37640	Sequence 37640, A
93	40	31.5	432	6	US-10-449-902-54770	Sequence 54770, A
94	40	31.5	432	6	US-10-449-902-55414	Sequence 55414, A
95	40	31.5	508	6	US-10-449-902-44377	Sequence 44377, A
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97	40	31.5	535	6	US-10-449-902-41243	Sequence 41243, A
98	40	31.5	708	7	US-11-258-767-16	Sequence 16, Appli

99 40 31.5 708 7 US-11-258-767-19 Sequence 19, Appl  
100 40 31.5 708 7 US-11-258-767-22 Sequence 22, Appl

## ALIGNMENTS

RESULT 1  
US-11-214-588-23  
; Sequence 23, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 23  
; LENGTH: 26  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-214-588-23

Query Match 100.0%; Score 127; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVALLPAVLLALLAPKNNLKECGLY 26  
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Db 1 AAVALLPAVLLALLAPKNNLKECGLY 26

RESULT 2  
US-11-214-588-24  
; Sequence 24, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 24  
; LENGTH: 26  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; NAME/KEY: BINDING  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: N-terminal amino acid is succinylated  
US-11-214-588-24

Query Match 100.0%; Score 127; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVALLPAVLLALLAPKNNLKECGLY 26  
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Db 1 AAVALLPAVLLALLAPKNNLKECGLY 26

RESULT 3  
US-11-214-588-26  
; Sequence 26, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 26  
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; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; NAME/KEY: BINDING  
; LOCATION: (17)..(26)  
; OTHER INFORMATION: A bond exists between the side chain of K at position 17 and the  
; OTHER INFORMATION: c-terminus of the peptide  
US-11-214-588-26

Query Match 100.0%; Score 127; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAVALLPAVLLALLAPKNNLKECGLY 26

RESULT 4  
US-11-214-588-29  
; Sequence 29, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 29  
; LENGTH: 26  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-214-588-29

Query Match 100.0%; Score 127; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 10, 2006, 16:50:59 ; Search time 12.5806 Seconds  
(without alignments)  
198.848 Million cell updates/sec

Title: US-10-009-809-7

Perfect score: 127

Sequence: 1 AAVALLPAVLLALLAPKNKLKCGLY 26

Scoring table: BLOSUM62

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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	63	49.6	206	2 JC4268	fibroblast growth
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4	57	44.9	354	1 RGHUI3	GTP-binding regula
5	57	44.9	354	1 RGTI13	GTP-binding regula
6	57	44.9	354	2 S28159	GTP-binding regula
7	57	44.9	354	2 S40508	GTP-binding regula
8	57	44.9	354	2 S40509	G-protein - chicke
9	52	40.9	5825	2 T12117	polyprotein - fava
10	50	39.4	354	1 RGH011	GTP-binding regula
11	50	39.4	354	1 RGHUI1	GTP-binding regula
12	50	39.4	354	1 RGTI11	GTP-binding regula
13	50	39.4	354	1 RGLI11	GTP-binding regula
14	50	39.4	354	2 S28157	GTP-binding regula
15	50	39.4	354	2 S24362	GTP-binding regula
16	50	39.4	354	2 I50237	GTP-binding regula
17	50	39.4	354	2 S27013	GTP-binding regula
18	50	39.4	355	1 RGHUI2	GTP-binding regula
19	50	39.4	355	1 RGHUI2	GTP-binding regula
20	50	39.4	355	1 RGTI12	GTP-binding regula
21	50	39.4	355	2 S28158	GTP-binding regula
22	50	39.4	355	2 I50238	GTP-binding regula
23	50	39.4	355	2 A61031	GTP-binding regula
24	50	39.4	355	2 A48976	GTP-binding regula
25	49	38.6	194	2 I50710	fibroblast growth
26	49	38.6	447	2 B82490	probable Na+/H+ an
27	48.5	38.2	763	2 A00170	probable membrane
28	48	37.8	443	2 T45574	anthranilate N-hyd
29	48	37.8	469	2 C71373	probable oxaloacet

30	47	37.0	317	2	E83344	probable adhesion
31	47	37.0	365	2	A71410	hypothetical prote
32	47	37.0	542	2	S30884	SRP1 protein - yea
33	46.5	36.6	156	2	H89455	tungsten formylmet
34	46	36.2	148	2	E89151	formate hydrogenly
35	46	36.2	181	1	KNPMS2	protein S2 - garde
36	46	36.2	345	1	RGLI13	GTP-binding regula
37	46	36.2	544	2	S61985	ALG6 protein - yea
38	45.5	35.8	397	2	A83999	mutants block spor
39	45	35.4	104	2	B25888	probable GTP-bind
40	45	35.4	128	2	I89024	MHC sex-limited pr
41	45	35.4	177	2	AH1232	hypothetical prote
42	45	35.4	347	2	A75537	hypothetical prote
43	45	35.4	357	2	T24992	hypothetical prote
44	45	35.4	411	1	S37643	protein kinase MSK
45	45	35.4	488	2	S13423	stromelysin 3 (EC
46	45	35.4	940	2	H71409	hypothetical prote
47	45	35.4	1735	2	S54784	sex-limited protei
48	45	35.4	1736	2	A29176	sex-limited protei
49	45	35.4	1738	1	A24558	complement C4 prec
50	44.5	35.0	962	2	D70661	probable membranep
51	44	34.6	74	2	D84231	hypothetical prote
52	44	34.6	132	2	S04830	regulatory protein
53	44	34.6	261	2	T37948	probable U1 small
54	44	34.6	273	2	B89884	hypothetical prote
55	44	34.6	300	2	S69028	probable membrane
56	44	34.6	334	2	G84123	iron (III) dicitra
57	44	34.6	350	1	RGBOT1	GTP-binding regula
58	44	34.6	350	1	RGHUT1	GTP-binding regula
59	44	34.6	350	1	RGHUT1	GTP-binding regula
60	44	34.6	354	1	RGBOT2	GTP-binding regula
61	44	34.6	354	1	RGHUT2	GTP-binding regula
62	44	34.6	354	2	S24352	GTP-binding regula
63	44	34.6	406	2	T04613	gustducin - rat
64	44	34.6	412	1	S37642	hypothetical prote
65	44	34.6	682	2	T50840	protein kinase MSK
66	44	34.6	683	2	T50839	U4/U6-associated R
67	44	34.6	1089	2	T45766	U4/U6 small nuclea
68	44	34.6	1094	2	F70697	nosa protein - bli
69	44	34.6	1459	2	S50437	probable arabinosy
70	44	34.6	1557	2	T28811	hypothetical prote
71	43.5	34.3	433	2	D82280	hypothetical prote
72	43.5	34.3	833	2	S50225	oxaloacetate decar
73	43.5	34.3	1630	2	T00390	potassium transpor
74	43	33.9	120	2	T44554	KIAA0614 protein -
75	43	33.9	151	2	S75779	hypothetical prote
76	43	33.9	238	1	S19012	hypothetical prote
77	43	33.9	265	2	A83969	licheninase (EC 3.
78	43	33.9	292	2	T22665	hypothetical prote
79	43	33.9	451	2	B82488	hypothetical prote
80	43	33.9	526	2	E86149	ATP-dependent RNA
81	43	33.9	557	2	T49811	T1N6.20 protein -
82	43	33.9	625	2	T21051	probable vacuolar
83	43	33.9	660	2	E85499	hypothetical prote
84	43	33.9	660	2	E90648	hypothetical prote
85	43	33.9	660	2	A64739	ferrichrome-iron t
86	43	33.9	788	2	S48191	probable ubiquinol
87	43	33.9	852	2	A72343	hypothetical prote
88	43	33.9	1051	2	JC4051	glycoprotein A - p
89	43	33.9	1251	2	A57293	latent transformati
90	43	33.9	1462	2	T11648	probable mitotic s
91	43	33.9	4550	2	T18440	hypothetical prote
92	42.5	33.5	303	2	B81348	binding-protein de
93	42.5	33.5	410	2	A83407	probable amino aci
94	42.5	33.5	520	2	C89980	hypothetical prote
95	42.5	33.5	799	2	B71478	probable cell divi
96	42	33.1	130	1	KNPMP4	protein P4 - garde
97	42	33.1	191	2	B71814	thymidylate kinase
98	42	33.1	191	2	B64704	thymidylate kinase
99	42	33.1	196	2	S16017	shoot-specific pro
100	42	33.1	199	2	T40079	hypothetical prote

## ALIGNMENTS

```
RESULT 1
TVHUHS
fibroblast growth factor 4 - human
N;Alternate names: heparin secretory transforming protein 1; Kaposi sarcoma oncogene; th
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A28417; A29676; A29649
R;Yoshida, T.; Miyagawa, K.; Odagiri, H.; Sakamoto, H.; Little, P.F.R.; Terada, M.; Sug
Proc. Natl. Acad. Sci. U.S.A. 84, 7305-7309, 1987
A;Title: Genomic sequence of hst, a transforming gene encoding a protein homologous to f
A;Reference number: A28417; MUID:88041096; PMID:2959959
A;Accession: A28417
A;Molecule type: DNA
A;Residues: 1-206 <YOS>
A;Cross-references: UNIPROT:P08620; UNIPARC:UPI0000040662; DDBJ:J02986; NID:g184430; PID
R;Taira, M.; Yoshida, T.; Miyagawa, K.; Sakamoto, H.; Terada, M.; Sugimura, I.
Proc. Natl. Acad. Sci. U.S.A. 84, 2980-2984, 1987
A;Title: cDNA sequence of human transforming gene hst and identification of the coding s
A;Reference number: A29876; MUID:87204251; PMID:2953031
A;Accession: A29876
A;Molecule type: mRNA
A;Residues: 1-206 <TAI>
A;Cross-references: UNIPARC:UPI0000040662; GB:J02986; GB:M16338; NID:g184430; PIDN:AAB59
R;Delli Bovi, P.; Curatola, A.M.; Kern, F.G.; Greco, A.; Ittmann, M.; Basilico, C.
Cell 50, 729-737, 1987
A;Title: An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes a growth f
A;Reference number: A29649; MUID:87301716; PMID:2957062
A;Accession: A29649
A;Molecule type: mRNA
A;Residues: 1-206 <BOV>
A;Cross-references: UNIPARC:UPI0000040662; GB:M17446; NID:g186785; PIDN:AAA59473.1; PID:
C;Comment: This protein is an oncogene for Kaposi's sarcoma. It is homologous to the mou
C;Genetics:
A;Gene: GDB:FGF4; HSPF1
A;Cross-references: GDB:120066; OMIM:164980
A;Map position: 11q13.3-11q13.3
A;Introns: 114/1; 148/3
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; Kaposi sarcoma; transforming protein

Query Match 55.1%; Score 70; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVALLPAVLALLAP 16
| | | | | | | | | | | | | | | |
Db 7 AAVALLPAVLALLAP 22

RESULT 2
JC4268
fibroblast growth factor 4 - bovine
N;Alternate names: transforming protein hst
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 17-Mar-2000
C;Accession: JC4268
R;Yu, J.C.; DeSeabra, A.J.J.; Wang, L.M.; Fleming, T.P.; Chedid, M.; Miki, T.; Heidaran,
Gene 162, 333-334, 1995
A;Title: An unexpected transforming gene in calf-thymus carrier DNA: Bovine hst.
A;Reference number: JC4268; MUID:96032369; PMID:7557455
A;Accession: JC4268
A;Molecule type: mRNA
A;Residues: 1-206 <YLU>
A;Cross-references: UNIPARC:UPI0000176539; GB:U15969
A;Note: The authors translated the codon GGC for residue 114 as Ser
C;Comment: This protein is a member of fibroblast growth factor family. The hstgene in c
C;Genetics:
A;Gene: hst
A;Introns: 113/3; 145/2
C;Superfamily: fibroblast growth factor
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## C;Keywords: thymus; transforming protein

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Query Match 49.6%; Score 63; DB 2; Length 206;
Best Local Similarity 87.5%; Pred. No. 0.073;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAVALLPAVLALLAP 16
| | | | | | | | | | | | | | | |
Db 7 AAVALLPAVLALLAP 22

RESULT 3
I48071
GTP binding protein - Chinese hamster (fragment)
C;Species: Cricetus griseus (Chinese hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48071
R;Baron, B.; Fernandez, M.A.; Toledo, F.; Le Roscouet, D.; Mayau, V.; Martin, N.; Buttin
Genomics 24, 288-294, 1994
A;Title: The highly conserved Chinese hamster GNAI3 gene maps less than 60 kb from the A
A;Reference number: I48071; MUID:95213019; PMID:7698751
A;Accession: I48071
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-63 <RES>
A;Cross-references: UNIPROT:Q60397; UNIPARC:UPI0000012B20; EMBL:X79282; NID:g642170; PID
C;Genetics:
A;Gene: Galphai3
C;Superfamily: GTP-binding regulatory protein Gs alpha chain

Query Match 44.9%; Score 57; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 KNNLKEGGLY 26
| | | | | | | | | | | | | | | |
Db 54 KNNLKEGGLY 63

RESULT 4
RGHUI3
GTP-binding regulatory protein Gi alpha-3 chain (adenylate cyclase-inhibiting) - human
N;Alternate names: GTP-binding regulatory protein Gk alpha chain; guanine nucleotide bin
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: S02348; S00055; A32139; C28154; A28157; S00078
R;Beals, C.R.; Wilson, C.B.; Perlmutter, R.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 7886-7890, 1987
A;Title: A small multigene family encodes G(i) signal-transduction proteins.
A;Reference number: S02319; MUID:8808503; PMID:3120178
A;Accession: S02348
A;Molecule type: mRNA
A;Residues: 1-354 <BEA>
A;Cross-references: UNIPROT:P08754; UNIPARC:UPI000004D205; EMBL:J03005; NID:g183183; PID
R;Didsbury, J.R.; Snyderman, R.
FEBS Lett. 219, 259-263, 1987
A;Title: Molecular cloning of a new human G protein. Evidence for two G(i-alpha)-like pr
A;Reference number: S00055; MUID:87247315; PMID:3109953
A;Accession: S00055
A;Molecule type: mRNA
A;Residues: 1-354 <DID>
A;Cross-references: UNIPARC:UPI000004D205; EMBL:M27543; NID:g183395; PIDN:AAAS2579.1; PI
R;Kim, S.; Ang, S.L.; Bloch, D.B.; Bloch, K.D.; Kawahara, Y.; Tolman, C.; Lee, R.; Seidm
Proc. Natl. Acad. Sci. U.S.A. 85, 4153-4157, 1988
A;Title: Identification of cDNA encoding an additional alpha-subunit of a human GTP-bind
A;Reference number: A32139; MUID:88247980; PMID:3132707
A;Accession: A32139
A;Molecule type: mRNA
A;Residues: 1-354 <KIM>
A;Cross-references: UNIPARC:UPI000004D205; GB:J03238; NID:g183686; PIDN:AAA35939.1; PID:
R;Itch, H.; Toyama, R.; Kozasa, T.; Tsukamoto, T.; Matsuo, M.; Kaziro, Y.
J. Biol. Chem. 263, 6656-6664, 1988
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GenCore version 5.1.1.9

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:50:27 ; Search time 96.0323 Seconds  
(without alignments)  
250.441 Million cell updates/sec

Title: US-10-009-809-7

Perfect score: 127

Sequence: 1 AAVALLPAVILLALLAPKNLKECGLY 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	55.1	206	1 FGF4_HUMAN	P48620 homo sapien
2	63	49.6	206	1 FGF4_BOVIN	P48803 bos taurus
3	57	44.9	63	1 GNAI3_CRIGR	Q60397 cricetus
4	57	44.9	89	2 Q8QG22_FUGRU	Q8QG22 fugu rubrip
5	57	44.9	329	2 Q3J3B3_RHOS4	Q3J3B3 rhodobacter
6	57	44.9	346	2 Q45QMR_RAT	Q45QMR rattus norv
7	57	44.9	353	1 GNAI3_CAVPO	Q98403 cavia porce
8	57	44.9	353	1 GNAI3_HUMAN	P08754 homo sapien
9	57	44.9	353	1 GNAI3_MOUSE	Q98C51 mus musculu
10	57	44.9	353	1 GNAI3_RAT	P08753 rattus norv
11	57	44.9	354	2 Q5TZX1_HUMAN	O5TZX1 homo sapien
12	57	44.9	354	2 Q3ZCAT_BOVIN	Q3ZCAT bos taurus
13	57	44.9	354	2 Q3HR12_CRIGR	Q3HR12 cricetus
14	57	44.9	354	2 Q3TGVI_MOUSE	Q3TGVI mus musculu
15	57	44.9	354	2 Q3TJH1_MOUSE	Q3TJH1 mus musculu
16	57	44.9	354	2 Q90846_CHICK	Q90846 gallus gall
17	57	44.9	354	2 Q30847_CHICK	Q30847 gallus gall
18	56	44.1	480	2 Q33WH1_9GAMM	Q33WH1 shewanella
19	55	43.3	439	2 Q2SLD2_9GAMM	Q2SLD2 shewanella
20	55	43.3	445	2 Q3QK98_9GAMM	Q3QK98 shewanella
21	55	43.3	871	2 Q3W5H3_9ACTO	Q3W5H3 frankia sp.
22	55	43.3	1016	1 CMTA4_ARATH	Q9FYG2 arabidopsis
23	53	41.7	444	2 Q3Q5U7_9GAMM	Q3Q5U7 shewanella
24	53	41.7	445	2 Q2ZV10_SHEPU	Q2ZV10 shewanella
25	53	41.7	462	2 Q2X738_9GAMM	Q2X738 shewanella
26	53	41.7	1956	2 Q7QSUI_GIALA	Q7QSUI giardia lam
27	52.5	41.3	386	2 Q440C5_SOLUS	Q440C5 solibacter
28	52	40.9	445	2 Q224S0_9GAMM	Q224S0 shewanella
29	52	40.9	445	2 Q35V04_9GAMM	Q35V04 shewanella
30	52	40.9	445	2 Q368E6_9GAMM	Q368E6 shewanella
31	52	40.9	449	2 Q3P3U7_9GAMM	Q3P3U7 shewanella

## ALIGNMENTS

32	52	40.9	718	2	Q9F544_ECOLI	Q9F544 escherichia
33	52	40.9	5825	2	O82731_STVIRU	O82731 vicia faba
34	51	40.2	206	2	O9KZV1_STRCO	O9KZV1 streptomyce
35	51	40.2	451	2	O6LNC2_PHOPR	O6LNC2 photobacter
36	51	40.2	479	2	O45R98_STRFR	O45R98 streptomyce
37	50.5	39.8	97	2	Q4W8Y1_ASFFU	Q4W8Y1 aspergillus
38	50	39.4	53	2	Q922Y6_MOUSE	Q922Y6 mus musculu
39	50	39.4	132	2	Q8JZT4_MOUSE	Q8JZT4 mus musculu
40	50	39.4	157	2	O6LCB5_HUMAN	O6LCB5 homo sapien
41	50	39.4	221	2	O72Q04_LEPIC	O72Q04 leptospira
42	50	39.4	221	2	O8F671_LEPIN	O8F671 leptospira
43	50	39.4	270	2	Q2JUN9_9CYAN	Q2JUN9 cyanobacter
44	50	39.4	301	2	Q9Y206_HYDMA	Q9Y206 hydra magni
45	50	39.4	347	2	O7ZW15_BRARE	O7ZW15 brachydanio
46	50	39.4	353	1	GNAI1_BOVIN	P63097 bos taurus
47	50	39.4	353	1	GNAI1_CAVPO	P38401 cavia porce
48	50	39.4	353	1	GNAI1_CHICK	P38401 gallus gall
49	50	39.4	353	1	GNAI1_HUMAN	P63096 homo sapien
50	50	39.4	353	1	GNAI1_ORYLA	P87383 oryzias lat
51	50	39.4	353	1	GNAI1_PONPY	Q5RAD4 pongo pygma
52	50	39.4	353	1	GNAI1_RAT	P10824 rattus norv
53	50	39.4	353	1	GNAI1_XENLA	P27044 xenopus lae
54	50	39.4	353	1	GNAI1_ASTPE	P30676 asterina pe
55	50	39.4	353	1	GNAI1_HELTI	P51876 helisoma tr
56	50	39.4	353	1	GNAI1_LYMSI	P30682 lymanea sta
57	50	39.4	353	2	Q5DBN1_SCHJA	Q5DBN1 schistosoma
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59	50	39.4	353	2	O5R9N4_PONPY	O5R9N4 pongo pygma
60	50	39.4	354	1	GNAI2_CAVPA	P38400 canis famli
61	50	39.4	354	1	GNAI2_CAVPO	P38402 cavia porce
62	50	39.4	354	1	GNAI2_CHICK	P50147 gallus gall
63	50	39.4	354	1	GNAI2_HUMAN	P04899 homo sapien
64	50	39.4	354	1	GNAI2_MACFA	Q4T592 macaca fasc
65	50	39.4	354	1	GNAI2_MOUSE	P08752 mus musculu
66	50	39.4	354	1	GNAI2_ORYLA	O13055 oryzias lat
67	50	39.4	354	1	GNAI2_RAT	P04897 rattus norv
68	50	39.4	354	1	GNAI1_HOMAM	P41776 homarus ame
69	50	39.4	354	2	Q6QM16_LYTVA	Q6QM16 lytechinus
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71	50	39.4	354	2	O8WP45_HALRO	O8WP45 halocynthia
72	50	39.4	354	2	Q8WSS1_CIOIN	Q8WSS1 ciona intes
73	50	39.4	354	2	Q8WSS2_CIOIN	Q8WSS2 ciona intes
74	50	39.4	354	2	Q9NL94_OCTUV	Q9NL94 octopus vul
75	50	39.4	354	2	Q2KJCO_BOVIN	Q2KJCO bos taurus
76	50	39.4	354	2	Q3LRD4_CRIGR	Q3LRD4 cricetus
77	50	39.4	354	2	Q45QMR_RAT	Q45QMR rattus norv
78	50	39.4	354	2	Q4S710_TETNG	Q4S710 tetraodon n
79	50	39.4	354	2	Q6GPC5_XENLA	Q6GPC5 xenopus lae
80	50	39.4	354	2	Q7T3D3_BRARE	Q7T3D3 brachydanio
81	50	39.4	355	2	Q96C71_BRARE	Q96C71 homo sapien
82	50	39.4	355	2	Q3HR13_CRIGR	Q3HR13 cricetus
83	50	39.4	355	2	Q3TXK7_MOUSE	Q3TXK7 m osteoclas
84	50	39.4	355	2	Q45QNO_RAT	Q45QNO rattus norv
85	50	39.4	355	2	Q5U4X0_XENLA	Q5U4X0 xenopus lae
86	50	39.4	355	2	Q6P3M7_XENTR	Q6P3M7 xenopus tro
87	50	39.4	355	2	Q6TNT8_BRARE	Q6TNT8 brachydanio
88	50	39.4	355	2	Q9W6A4_SQUAC	Q9W6A4 squalus aca
89	50	39.4	370	2	Q33H49_METHU	Q33H49 methanospir
90	50	39.4	377	2	Q7ZW82_BRARE	Q7ZW82 brachydanio
91	50	39.4	404	2	Q4SACO_TETNG	Q4SACO tetraodon n
92	50	39.4	437	2	Q3IKQ8_PSEHT	Q3IKQ8 pseudaalter
93	50	39.4	499	2	Q4RXT7_TETNG	Q4RXT7 tetraodon n
94	49.5	39.0	285	2	Q72FG9_DESVH	Q72FG9 desulfovibr
95	49	38.6	194	1	EGF4_CHICK	P48804 gallus gall
96	49	38.6	293	2	Q3FIG7_9BURK	Q3FIG7 burkholderi
97	49	38.6	293	2	Q45BK3_9BURK	Q45BK3 burkholderi
98	49	38.6	293	2	Q4LYT6_9BURK	Q4LYT6 burkholderi
99	49	38.6	447	2	Q9KMX3_VIBCH	Q9KMX3 vibrio chol
100	48.5	38.2	763	2	Q74VT3_YERPE	Q74VT3 yersinia pe

```

RESULT 1
FGF4_HUMAN STANDARD; PRT; 206 AA.
AC P08620;
DT 01-AUG-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1988, sequence version 1.
DT 07-FEB-2006, entry version 60.
DE Fibroblast growth factor 4 precursor (FGF-4) (Heparin secretory
DE transforming protein) (HST-1) (HST) (Transforming protein KS3) (HBGF-
DE 4).
GN Name=FGF4; Synonyms=HST, HSTF1, KS3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88041096; PubMed=2959959;
RA Yoshida T., Miyagawa K., Odagiri H., Sakamoto H., Little P.F.R.,
RA Terada M., Sugimura T.;
RT "Genomic sequence of hst, a transforming gene encoding a protein
RT homologous to fibroblast growth factors and the int-2-encoded
RT protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7305-7309(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87204251; PubMed=2953031;
RA Taira M., Yoshida T., Miyagawa K., Sakamoto H., Terada M.,
RA Sugimura T.;
RT "cDNA sequence of human transforming gene hst and identification of
RT the coding sequence required for transforming activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2980-2984(1987).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87301716; PubMed=2957062; DOI=10.1016/0092-8674(87)90331-X;
RA Delli Bovi P., Curatola A.M., Kern F.G., Greco A., Iltmann M.,
RA Basiglio C.;
RT "An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes
RT a growth factor that is a member of the FGF family.";
RL Cell 50:729-737(1987).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 79-206.
RX MEDLINE=21378624; PubMed=11485033;
RA DOI=10.1126/SCIENCE.21.17.5946-5957.2001;
RA Bellosa P., Iwahori A., Plotnikov A.N., Eliseenkova A.V.,
RA Basiglio C., Mohammadi M.;
RT "Identification of receptor and heparin binding sites in fibroblast
RT growth factor 4 by structure-based mutagenesis.";
RL Mol. Cell. Biol. 21:5946-5957(2001).
CC -!- FUNCTION: Can transform NIH 3T3 cells from a human stomach tumor
CC (het) and from Kaposi's sarcoma (KS3). It has a mitogenic
CC activity.
CC
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC -----
CC EMBL: J02986; AA059555.1; -; Genomic_DNA.
CC EMBL: M17446; AA59473.1; -; mRNA.
CC PIR: A28417; TVRHUS.
CC DR PDB: 1IJT; X-ray; A:79-206.
CC DR Ensembl: ENSG00000075388; Homo sapiens.
CC DR HGNC: HGNC:3682; FGF4.
CC DR MIM: 164980; gene.
CC DR GO: GO:0005576; C:extracellular region; TAS.
CC DR GO: GO:0008083; F:growth factor activity; TAS.
CC DR GO: GO:0007267; P:cell-cell signaling; TAS.
CC DR GO: GO:0008284; P:positive regulation of cell proliferation; TAS.
CC DR GO: GO:0007165; P:signal transduction; TAS.
CC DR InterPro: IPR002209; GF heparin_bf.
CC DR InterPro: IPR002348; IL1_HBGF.

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DR Pfam: PF00167; FGF; 1.
DR PRINTS; PR00263; HBGF; FGF.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW 3D-structure; Growth factor; Heparin-binding; Mitogen; Proto-oncogene;
KW Signal.
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FT CHAIN 1 30 Potential.
FT CHAIN 31 206 Fibroblast growth factor 4.
FT /FTID=PRO_000008953.
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FT STRAND 82 88
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FT STRAND 112 114
FT HELIX 116 122
FT TURN 123 124
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FT TURN 131 134
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FT TURN 153 154
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FT HELIX 163 165
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Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAVALLPAVLLALLAP 16
Db 7 AAVALLPAVLLALLAP 22
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| | | | | | | | | | | | | | | |
RESULT 2
FGF4_BOVIN STANDARD; PRT; 206 AA.
AC P48803;
DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1996, sequence version 1.
DT 07-FEB-2006, entry version 38.
DE Fibroblast growth factor 4 precursor (FGF-4) (Heparin secretory
DE transforming protein) (HST) (HBGF-4).
GN Name=FGF4; Synonyms=HST;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Thymus;
RX MEDLINE=96032369; PubMed=7557455; DOI=10.1016/0378-1119(95)00330-9;
RA Yu J.C., Deeeabra A.J., Fleming T.P., Chedid M., Miki T.,
RA Heidaran M.A.;
RT "An unexpected transforming gene in calf-thymus carrier DNA: bovine

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:55:58 ; Search time 58 Seconds  
(without alignments)  
78.830 Million cell updates/sec

Title: US-10-009-809-1

Perfect score: 57

Sequence: 1 KNNLKECGLY 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 606527

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A Geneseq\_8.\*

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- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*
- 10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	57	100.0	10	5	Aae26131 Galphai3
2	57	100.0	10	5	Aae26129 Galphai3
3	52	91.2	10	5	Aae26134 Anti-alle
4	51	89.5	10	5	Aae26133 Anti-alle
5	51	89.5	10	5	Aae26136 Anti-alle
6	50	87.7	10	2	Aar61259 Control p
7	50	87.7	10	2	Aar49785 Farnesylt
8	50	87.7	10	2	Aar04476 Weak inh
9	50	87.7	10	5	Aae26132 Anti-alle
10	50	87.7	10	5	Aae26151 Galphai2
11	47	82.5	10	5	Aae26135 Anti-alle
12	47	82.5	10	5	Aae26152 Peptide d
13	44	77.2	10	1	Aap82558 Guanine n
14	44	77.2	10	5	Aae26130 Galphat d
15	42	73.7	10	1	Aap82561 Guanine n
16	33	57.9	7	7	Abw00034 Human G a
17	33	57.9	9	7	Ade68698 Human 161
18	31	54.4	5	6	Aao26779 Galphas C
19	31	54.4	5	9	Adz88296 Chimeric
20	31	54.4	5	10	Aee97653 LPSR1 ass
21	31	54.4	9	7	Ade67532 Human 161
22	31	54.4	9	7	Ade69088 Human 161
23	31	54.4	9	7	Ade68274 Human 161

Ad666418	Human 161	7	Ad666418
Ad669278	Human 161	10	Ad669278
Adn67888	Human 273	9	Adn67888
Adn69294	Human 273	9	Adn69294
Adn66092	Human 273	9	Adn66092
Adn67026	Human 273	9	Adn67026
Adn68445	Human 273	9	Adn68445
Adn68871	Human 273	9	Adn68871
Adn66899	Human 273	9	Adn66899
Adn69516	Human 273	9	Adn69516
Abb51637	Human 34P	10	Abb51637
Adn69944	Human 273	10	Adn69944
Adn69733	Human 273	10	Adn69733
Adn69991	Human 273	10	Adn69991
Adn70462	Human 273	10	Adn70462
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Abu13803	Modified	5	Abu13803
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Abb51554	Human 34P	9	Abb51554
Abb51754	Human 34P	9	Abb51754
Abb51351	Human 34P	9	Abb51351
Abb51552	Human 34P	9	Abb51552
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Ad66562	Human 161	9	Ad66562
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Ad668507	Human 161	9	Ad668507
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Aae24129	Rice CO39	8	Aae24129
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Abb51675	Human 34P	9	Abb51675
Aau93433	Granulocy	9	Aau93433
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97 25 43.9 9 9 AEC97844 Rec97844 HLA-A24-b  
98 25 43.9 10 4 AAB51144 Aab51144 Human man  
99 25 43.9 10 5 ABG94682 Abg94682 Human man  
100 25 43.9 10 7 ABW00065 Abw00065 Human man

## ALIGNMENTS

RESULT 1  
AAE26131  
ID AAE26131 standard; peptide; 10 AA.  
XX AAE26131;  
XX 14-NOV-2002 (first entry)  
XX Galphai3 cyclic peptide.  
DE  
XX Antiallergic agent; nasal allergy; eye; skin; acute urticaria; psoriasis;  
KW psychogenic; allergic asthma; interstitial cystitis; bowel disease;  
KW multiple sclerosis; dermatological; antiinflammatory; neuroprotective;  
KW migraine; cyclic.  
OS Unidentified.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 1 /note= "This residue is linked to Tyr at position 10 by  
FT epsilon-NH"  
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FT Misc-difference 10 /note= "This residue is linked to Lys at position 1 by  
FT epsilon-NH"  
FT  
XX WO200250097-A2.  
XX  
XX 27-JUN-2002.  
XX  
XX 20-DEC-2001; 2001WO-IL001186.  
XX  
XX 21-DEC-2000; 2000IL-00140473.  
XX (ALLE-) ALLERGENE LTD.  
XX Eisenberg R, Raz T;  
PI  
XX WPI; 2002-636474/68.  
XX  
XX New antiallergic agent having first cell penetrating segment joined to  
PT antiallergic decapeptide providing antiallergic effect within mast cells,  
PT through linker which provides bend or turn at junction between segments.  
XX  
XX Claim 8; Page 57; 81pp; English.  
XX The invention relates to an antiallergic agent, comprising a complex  
CC molecule having at least a first segment competent for importation of the  
CC molecule into mast cells, joined to a second segment through a linker,  
CC where the second segment is the anti-allergic decapeptide derived from  
CC Galphai 3, providing antiallergic effect within mast cells, and linker  
CC provides a bend or turn at or near junction between the two segments. The  
CC invention is useful for treating allergic conditions such as nasal  
CC allergy, allergic reactions in an eye of the subject, allergic reactions  
CC in the skin of the subject, acute urticaria, psoriasis, psychogenic or  
CC allergic asthma, interstitial cystitis, bowel diseases, migraines or  
CC multiple sclerosis. The invention is also useful for preventing late  
CC phase inflammatory responses induced by protein kinase activation,  
CC preferably mitogen activated protein kinase activation, where the  
CC antiallergic agent is peptide 2, peptide 2-Succ and peptide 2-Cyc. The  
CC invention provides specific direct and targeted treatment of allergies  
CC and related inflammatory conditions. The present sequence is Galphai3  
cyclic peptide  
XX  
XX Sequence 10 AA;

Query Match 100.0%; Score 57; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00099;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 KNNLKECGLY 10  
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ID AAE26129 standard; peptide; 10 AA.  
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XX Antiallergic agent; nasal allergy; eye; skin; acute urticaria; psoriasis;  
KW psychogenic; allergic asthma; interstitial cystitis; bowel disease;  
KW multiple sclerosis; dermatological; antiinflammatory; neuroprotective;  
KW migraine.  
XX Unidentified.  
OS  
XX WO200250097-A2.  
XX  
XX 27-JUN-2002.  
XX  
XX 20-DEC-2001; 2001WO-IL001186.  
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XX 21-DEC-2000; 2000IL-00140473.  
XX (ALLE-) ALLERGENE LTD.  
XX Eisenberg R, Raz T;  
PI  
XX WPI; 2002-636474/68.  
XX  
XX New antiallergic agent having first cell penetrating segment joined to  
PT antiallergic decapeptide providing antiallergic effect within mast cells,  
PT through linker which provides bend or turn at junction between segments.  
XX  
XX Claim 8; Page 57; 81pp; English.  
XX The invention relates to an antiallergic agent, comprising a complex  
CC molecule having at least a first segment competent for importation of the  
CC molecule into mast cells, joined to a second segment through a linker,  
CC where the second segment is the anti-allergic decapeptide derived from  
CC Galphai 3, providing antiallergic effect within mast cells, and linker  
CC provides a bend or turn at or near junction between the two segments. The  
CC invention is useful for treating allergic conditions such as nasal  
CC allergy, allergic reactions in an eye of the subject, allergic reactions  
CC in the skin of the subject, acute urticaria, psoriasis, psychogenic or  
CC allergic asthma, interstitial cystitis, bowel diseases, migraines or  
CC multiple sclerosis. The invention is also useful for preventing late  
CC phase inflammatory responses induced by protein kinase activation,  
CC preferably mitogen activated protein kinase activation, where the  
CC antiallergic agent is peptide 2, peptide 2-Succ and peptide 2-Cyc. The  
CC invention provides specific direct and targeted treatment of allergies  
CC and related inflammatory conditions. The present sequence is Galphai3  
decapeptide  
XX  
XX Sequence 10 AA;

Query Match 100.0%; Score 57; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00099;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNNLKECGLY 10  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:59:01 ; Search time 21 Seconds  
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41.681 Million cell updates/sec

Title: US-10-009-809-1

Perfect score: 57

Sequence: 1 KNNLKECGLY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 176806

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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3: /EMC Cellerai\_SIDS3/prodata/2/iaa/7\_COMB.pep.\*

4: /EMC Cellerai\_SIDS3/prodata/2/iaa/H\_COMB.pep.\*

5: /EMC Cellerai\_SIDS3/prodata/2/iaa/PTUS\_COMB.pep.\*

6: /EMC Cellerai\_SIDS3/prodata/2/iaa/RE\_COMB.pep.\*

7: /EMC Cellerai\_SIDS3/prodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	50	87.7	10	5	PCT-US94-01768-19
5	50	87.7	10	7	5428134-6
6	50	87.7	10	7	5436320-6
7	44	77.2	10	7	5428134-1
8	44	77.2	10	7	5428134-10
9	44	77.2	10	7	5436320-1
10	44	77.2	10	7	5436320-7
11	42	73.7	10	7	5428134-4
12	42	73.7	10	7	5436320-4
13	26	45.6	9	2	US-09-620-091-246
14	25	43.9	8	3	US-09-641-528B-6112
15	25	43.9	8	3	US-09-641-528B-6119
16	25	43.9	8	3	US-09-641-528B-14504
17	25	43.9	8	3	US-09-641-528B-14511
18	25	43.9	8	3	US-09-641-528B-27731
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21	25	43.9	9	2	US-09-620-091-239
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28	25	43.9	9	3	US-09-641-528B-49574	Sequence 49574, A
29	25	43.9	9	3	US-09-641-528B-51040	Sequence 51040, A
30	25	43.9	9	7	5310729-21	Patent No. 5310729
31	25	43.9	10	3	US-09-641-528B-6217	Sequence 6217, Ap
32	25	43.9	10	3	US-09-641-528B-10536	Sequence 10536, A
33	25	43.9	10	3	US-09-641-528B-19093	Sequence 19093, A
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54	24	42.1	10	2	US-09-336-447A-89	Sequence 89, Appl
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61	23.5	41.2	8	2	US-09-714-602-53	Sequence 53, Appl
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63	23	40.4	7	1	US-09-641-528B-119	Sequence 119, App
64	23	40.4	8	3	US-09-641-528B-4739	Sequence 4739, Ap
65	23	40.4	8	3	US-09-641-528B-4747	Sequence 4747, Ap
66	23	40.4	8	3	US-09-641-528B-11865	Sequence 11865, A
67	23	40.4	8	3	US-09-641-528B-13579	Sequence 13579, A
68	23	40.4	8	3	US-09-641-528B-17952	Sequence 17952, A
69	23	40.4	8	3	US-09-641-528B-17968	Sequence 17968, A
70	23	40.4	8	3	US-09-641-528B-17995	Sequence 17995, A
71	23	40.4	8	3	US-09-641-528B-19646	Sequence 19646, A
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76	23	40.4	8	3	US-09-641-528B-31824	Sequence 31824, A
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84	23	40.4	9	3	US-09-641-528B-17969	Sequence 17969, A
85	23	40.4	9	3	US-09-641-528B-17980	Sequence 17980, A
86	23	40.4	9	3	US-09-641-528B-17996	Sequence 17996, A
87	23	40.4	9	3	US-09-641-528B-19688	Sequence 19688, A
88	23	40.4	9	3	US-09-641-528B-24637	Sequence 24637, A
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90	23	40.4	9	3	US-09-641-528B-30444	Sequence 30444, A
91	23	40.4	9	3	US-09-641-528B-31702	Sequence 31702, A
92	23	40.4	9	3	US-09-641-528B-31738	Sequence 31738, A
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96	23	40.4	9	3	US-09-641-528B-39956	Sequence 39956, A
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ALIGNMENTS

RESULT 1  
US-08-019-073-19  
; Sequence 19, Application US/08019073  
; Patent No. 5559209  
; GENERAL INFORMATION:  
; APPLICANT: Nishimoto, Ikuro  
; TITLE OF INVENTION: REGULATOR REGIONS OF G  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/019,073  
; FILING DATE: 19930218  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/146001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-019-073-19

Query Match 87.7%; Score 50; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 0.008;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KNNLKECGLY 10  
Db 1 KNNLKDCGLF 10  
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RESULT 2  
US-08-429-964-50  
; Sequence 50, Application US/08429964  
; Patent No. 5962243  
; GENERAL INFORMATION:  
; APPLICANT: BROWN, MICHAEL S.  
; APPLICANT: GOLDSTEIN, JOSEPH L.  
; APPLICANT: REISS, YUVAL  
; APPLICANT: JAMES, GUY L.  
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL  
; TITLE OF INVENTION: TRANSFERASE INHIBITORS  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARNOLD, WHITE & DURKEE

; STREET: P.O. BOX 4433  
; CITY: HOUSTON  
; STATE: TEXAS  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/429,964  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/021,625  
; FILING DATE: 16-FEB-1993  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: US 07/822,011  
; FILING DATE: ABANDONED  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: PCT/US/91/02650  
; FILING DATE: 18-APR-1991  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: US 07/615,715  
; FILING DATE: 20-NOV-1990  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: US 07/510,706  
; FILING DATE: 18-APR-1990 (ABANDONED)  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PARKER, DAVID L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTSD:432/PAR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (713) 789-2679  
; TELEX: 79-0924  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-429-964-50

Query Match 87.7%; Score 50; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 0.008;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KNNLKECGLY 10  
Db 1 KNNLKDCGLF 10  
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RESULT 3  
PCT-US93-08062-50  
; Sequence 50, Application PC/TUS9308062  
; GENERAL INFORMATION:  
; APPLICANT:  
; SEQUENCE CHARACTERISTICS:  
; SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.  
; SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.  
; SEQUENCE CHARACTERISTICS: REISS, YUVAL  
; SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.  
; ADDRESSEE: METHODS AND COMPOSITIONS FOR  
; ADDRESSEE: THE IDENTIFICATION,  
; ADDRESSEE: CHARACTERIZATION AND  
; ADDRESSEE: INHIBITION OF  
; ADDRESSEE: FARNESYLTRANSFERASE  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARNOLD, WHITE & DURKEE

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 10, 2006, 17:00:16 ; Search time 42.5 Seconds  
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Title: US-10-009-809-1

Perfect score: 57

Sequence: 1 KNNKEGGLY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 284686

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main.\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	57	100.0	10	4	US-10-465-826-3
3	53	93.0	10	4	US-10-465-826-4
4	52	91.2	10	4	US-10-465-826-6
5	51	89.5	10	4	US-10-465-826-5
6	51	89.5	10	4	US-10-465-826-8
7	50	87.7	10	4	US-10-465-826-31
8	47	82.5	10	4	US-10-465-826-7
9	47	82.5	10	4	US-10-465-826-32
10	44	77.2	10	4	US-10-465-826-2
11	31	54.4	5	5	US-10-978-282-21
12	29	50.9	10	3	US-09-779-308-368
13	27	47.4	9	3	US-09-779-308-82
14	27	47.4	9	3	US-09-779-308-206
15	27	47.4	9	3	US-09-779-308-283
16	27	47.4	9	3	US-09-779-308-285
17	27	47.4	9	3	US-09-779-308-394
18	27	47.4	9	3	US-09-779-308-485
19	27	47.4	9	3	US-09-779-308-504
20	27	47.4	9	3	US-09-779-308-586
21	27	47.4	9	4	US-10-286-457-526
22	27	47.4	9	4	US-10-100-303A-118
23	27	47.4	10	3	US-09-779-308-19
24	27	47.4	10	3	US-09-779-308-128
25	27	47.4	10	3	US-09-779-308-227
26	27	47.4	10	3	US-09-779-308-231
27	27	47.4	10	3	US-09-779-308-420

28	27	47.4	10	4	US-10-062-109A-202	Sequence 202, App
29	27	47.4	10	4	US-10-062-109A-309	Sequence 309, App
30	27	47.4	10	4	US-10-005-480A-202	Sequence 202, App
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35	27	47.4	10	6	US-11-097-912-309	Sequence 309, App
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38	26	45.6	5	5	US-10-978-282-22	Sequence 22, Appl
39	26	45.6	8	4	US-10-459-262A-68	Sequence 68, Appl
40	26	45.6	9	3	US-09-779-308-406	Sequence 406, App
41	26	45.6	9	4	US-10-623-176-34	Sequence 34, Appl
42	26	45.6	9	4	US-10-623-176-36	Sequence 36, Appl
43	26	45.6	9	4	US-10-623-176-38	Sequence 38, Appl
44	26	45.6	9	4	US-10-611-440-85	Sequence 85, Appl
45	26	45.6	9	5	US-10-659-207-246	Sequence 246, App
46	26	45.6	9	5	US-10-363-205-270	Sequence 270, App
47	26	45.6	9	5	US-10-929-988-246	Sequence 246, App
48	26	45.6	10	3	US-09-779-308-633	Sequence 633, App
49	26	45.6	10	5	US-10-254-610A-32	Sequence 32, Appl
50	26	45.6	10	5	US-10-254-610A-33	Sequence 33, Appl
51	25	43.9	9	5	US-10-659-207-239	Sequence 239, App
52	25	43.9	9	5	US-10-659-207-258	Sequence 258, App
53	25	43.9	9	5	US-10-929-988-239	Sequence 239, App
54	25	43.9	9	5	US-10-929-988-258	Sequence 258, App
55	25	43.9	9	5	US-10-929-988-259	Sequence 259, App
56	25	43.9	9	6	US-11-116-144-260	Sequence 260, App
57	25	43.9	9	6	US-11-220-372-260	Sequence 260, App
58	25	43.9	10	3	US-09-757-417-44	Sequence 44, Appl
59	25	43.9	10	4	US-10-042-945-44	Sequence 44, Appl
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63	24	42.1	5	4	US-10-321-807-131	Sequence 131, App
64	24	42.1	5	4	US-10-314-048A-131	Sequence 131, App
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66	24	42.1	5	5	US-10-930-862-131	Sequence 131, App
67	24	42.1	5	5	US-10-978-282-20	Sequence 20, Appl
68	24	42.1	5	5	US-10-516-517-16	Sequence 16, Appl
69	24	42.1	5	5	US-09-908-322-90	Sequence 90, Appl
70	24	42.1	8	3	US-09-783-931-90	Sequence 90, Appl
71	24	42.1	8	3	US-10-688-276-23	Sequence 23, Appl
72	24	42.1	8	3	US-09-731-221-42	Sequence 42, Appl
73	24	42.1	9	3	US-09-793-451-53	Sequence 53, Appl
74	24	42.1	9	3	US-09-793-451-255	Sequence 255, App
75	24	42.1	9	3	US-09-793-451-359	Sequence 359, App
76	24	42.1	9	3	US-09-793-451-638	Sequence 638, App
77	24	42.1	9	3	US-09-793-451-659	Sequence 659, App
78	24	42.1	9	3	US-10-283-722-53	Sequence 53, Appl
79	24	42.1	9	4	US-10-283-722-255	Sequence 255, App
80	24	42.1	9	4	US-10-283-722-359	Sequence 359, App
81	24	42.1	9	4	US-10-283-722-638	Sequence 638, App
82	24	42.1	9	4	US-10-283-722-659	Sequence 659, App
83	24	42.1	9	4	US-10-283-903-53	Sequence 53, Appl
84	24	42.1	9	4	US-10-283-903-255	Sequence 255, App
85	24	42.1	9	4	US-10-283-903-359	Sequence 359, App
86	24	42.1	9	4	US-10-283-903-638	Sequence 638, App
87	24	42.1	9	4	US-10-283-903-659	Sequence 659, App
88	24	42.1	9	4	US-10-459-262A-65	Sequence 65, Appl
89	24	42.1	9	4	US-10-459-262A-70	Sequence 70, Appl
90	24	42.1	9	4	US-10-623-176-35	Sequence 35, Appl
91	24	42.1	9	4	US-10-623-176-37	Sequence 37, Appl
92	24	42.1	9	4	US-10-623-176-39	Sequence 39, Appl
93	24	42.1	9	4	US-10-483-994-1	Sequence 1, Appl
94	24	42.1	9	5	US-10-483-993-1	Sequence 1, Appl
95	24	42.1	9	5	US-10-659-207-247	Sequence 247, App
96	24	42.1	9	5	US-10-659-207-261	Sequence 261, App
97	24	42.1	9	5	US-10-497-516-1	Sequence 1, Appl
98	24	42.1	9	5	US-10-929-988-247	Sequence 247, App
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## ALIGNMENTS

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RESULT 1
US-10-465-826-1
; Sequence 1, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamar
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Decapeptide derived from Homo sapiens G-alpha-i3
US-10-465-826-1

Query Match      100.0%; Score 57; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNNLKECGLY 10
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Db      1 KNNLKECGLY 10

RESULT 2
US-10-465-826-3
; Sequence 3, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamar
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: BINDING
; LOCATION: (1)..(10)
; OTHER INFORMATION: A bond exists between the side chain of K at position 1 and the
; OTHER INFORMATION: -terminus of the peptide
US-10-465-826-3

Query Match      100.0%; Score 57; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNNLKECGLY 10
      |||||
Db      1 KNNLKECGLY 10

RESULT 3
US-10-465-826-4
; Sequence 4, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamar
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (10)..(10)
; OTHER INFORMATION: Para-amino Phenylalanine at position 10
US-10-465-826-4

Query Match      93.0%; Score 53; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0069;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNNLKECGLY 10
      |||||
Db      1 KNNLKECGLY 10

RESULT 4
US-10-465-826-6
; Sequence 6, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamar
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-465-826-6

Query Match      91.2%; Score 52; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNNLKECGLY 10
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Db      1 KNNLKECGLY 10

RESULT 3
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; Sequence 4, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamar
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (10)..(10)
; OTHER INFORMATION: Para-amino Phenylalanine at position 10
US-10-465-826-4

Query Match      93.0%; Score 53; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0069;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNNLKECGLY 10
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Db      1 KNNLKECGLY 10

RESULT 4
US-10-465-826-6
; Sequence 6, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamar
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-465-826-6

Query Match      91.2%; Score 52; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNNLKECGLY 10
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Db      1 KNNLKECGLY 10
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OM protein - protein search, using sw model

Run on: July 10, 2006, 17:01:46 ; Search time 12.5 Seconds  
(without alignments)  
21.466 Million cell updates/sec

Title: US-10-009-809-1

Perfect score: 57

Sequence: 1 KNNLKEGGLY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 10037

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /EMC\_Celettera\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
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6: /EMC\_Celettera\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /EMC\_Celettera\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /EMC\_Celettera\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	10	7	US-11-214-588-1
2	57	100.0	10	7	US-11-214-588-3
3	53	93.0	10	7	US-11-214-588-4
4	52	91.2	10	7	US-11-214-588-6
5	51	89.5	10	7	US-11-214-588-5
6	51	89.5	10	7	US-11-214-588-8
7	50	87.7	10	7	US-11-214-588-31
8	47	82.5	10	7	US-11-214-588-7
9	47	82.5	10	7	US-11-214-588-32
10	44	77.2	10	7	US-11-214-588-2
11	23	40.4	9	7	US-11-140-487A-395
12	23	40.4	9	7	US-11-140-487A-523
13	23	40.4	9	7	US-11-140-487A-613
14	23	40.4	10	7	US-11-122-986-622
15	22	38.6	9	6	US-10-538-066-622
16	21	36.8	8	6	US-10-538-066-411
17	21	36.8	9	6	US-10-538-066-179
18	21	36.8	9	6	US-10-538-066-180
19	21	36.8	9	6	US-10-538-066-412
20	21	36.8	9	6	US-10-953-613C-537
21	21	36.8	9	6	US-10-953-613C-538
22	21	36.8	9	7	US-11-140-487A-1250
23	21	36.8	10	7	US-11-183-325-41
24	20	35.1	5	7	US-11-264-784-373
25	20	35.1	5	7	US-11-264-737-222

26	20	35.1	5	7	US-11-265-761-404	Sequence 404, App
27	20	35.1	8	7	US-11-264-784-374	Sequence 374, App
28	20	35.1	8	7	US-11-264-784-375	Sequence 375, App
29	20	35.1	8	7	US-11-223-610-24	Sequence 24, Appl
30	20	35.1	8	7	US-11-264-737-223	Sequence 223, App
31	20	35.1	8	7	US-11-264-737-224	Sequence 224, App
32	20	35.1	8	7	US-11-265-761-405	Sequence 405, App
33	20	35.1	8	7	US-11-265-761-406	Sequence 406, App
34	20	35.1	9	7	US-11-140-487A-1179	Sequence 1179, Ap
35	20	35.1	9	7	US-11-140-487A-1627	Sequence 1627, Ap
36	20	35.1	10	7	US-11-140-487A-948	Sequence 948, App
37	19	33.3	4	7	US-11-199-062-55	Sequence 55, Appl
38	19	33.3	9	6	US-10-489-071-105	Sequence 105, App
39	19	33.3	9	6	US-10-489-071-108	Sequence 108, App
40	19	33.3	9	6	US-10-506-334-3	Sequence 3, Appl
41	19	33.3	9	6	US-10-506-334-20	Sequence 20, Appl
42	19	33.3	9	7	US-11-122-986-789	Sequence 789, App
43	19	33.3	9	7	US-11-332-378-65	Sequence 65, Appl
44	19	33.3	9	7	US-11-332-378-72	Sequence 72, Appl
45	19	33.3	9	7	US-11-332-378-124	Sequence 124, App
46	19	33.3	9	7	US-11-340-431-279	Sequence 279, App
47	19	33.3	9	7	US-11-257-818-58	Sequence 58, Appl
48	19	33.3	9	7	US-11-257-818-66	Sequence 66, Appl
49	19	33.3	10	6	US-10-489-071-43	Sequence 43, Appl
50	19	33.3	10	6	US-10-521-401A-23	Sequence 23, Appl
51	19	33.3	10	6	US-10-506-334-13	Sequence 13, Appl
52	19	33.3	10	6	US-10-506-334-24	Sequence 24, Appl
53	19	33.3	10	6	US-10-526-062-23	Sequence 23, Appl
54	19	33.3	10	7	US-11-024-544A-77	Sequence 77, Appl
55	19	33.3	10	7	US-11-140-487A-1526	Sequence 1526, Ap
56	19	33.3	10	7	US-11-190-750-56	Sequence 56, Appl
57	19	33.3	10	7	US-11-122-986-795	Sequence 795, App
58	18	31.6	8	7	US-11-099-283B-364	Sequence 364, App
59	18	31.6	9	7	US-11-140-487A-846	Sequence 846, App
60	18	31.6	9	7	US-11-140-487A-914	Sequence 914, App
61	18	31.6	9	7	US-11-140-487A-1246	Sequence 1246, Ap
62	18	31.6	9	7	US-11-140-487A-1251	Sequence 1251, Ap
63	18	31.6	9	7	US-11-140-487A-1675	Sequence 1675, Ap
64	18	31.6	9	7	US-11-140-487A-1676	Sequence 1676, Ap
65	18	31.6	9	7	US-11-140-487A-1864	Sequence 1864, Ap
66	18	31.6	9	7	US-11-140-487A-1961	Sequence 1961, Ap
67	18	31.6	9	7	US-11-140-487A-1962	Sequence 1962, Ap
68	18	31.6	9	7	US-11-223-610-87	Sequence 87, Appl
69	18	31.6	10	6	US-10-516-079-72	Sequence 72, Appl
70	18	31.6	10	6	US-10-516-079-73	Sequence 73, Appl
71	18	31.6	10	6	US-10-516-079-76	Sequence 76, Appl
72	18	31.6	10	7	US-11-140-487A-847	Sequence 847, App
73	18	31.6	10	7	US-11-140-487A-1877	Sequence 1877, Ap
74	18	31.6	10	7	US-11-318-939-1	Sequence 1, Appl
75	18	31.6	10	7	US-11-183-325-29	Sequence 29, Appl
76	18	31.6	10	7	US-11-355-444-3	Sequence 3, Appl
77	18	31.6	10	7	US-11-134-871-626	Sequence 626, App
78	18	31.6	10	7	US-11-134-871-2832	Sequence 2832, Ap
79	17	29.8	6	7	US-11-257-818-14	Sequence 14, Appl
80	17	29.8	7	6	US-10-546-594-4	Sequence 4, Appl
81	17	29.8	7	7	US-11-061-841-303	Sequence 303, App
82	17	29.8	7	1	US-09-949-925-253	Sequence 253, App
83	17	29.8	8	7	US-11-099-283B-238	Sequence 238, App
84	17	29.8	9	6	US-10-489-071-77	Sequence 77, Appl
85	17	29.8	9	6	US-10-489-071-109	Sequence 109, App
86	17	29.8	9	6	US-10-489-071-140	Sequence 140, App
87	17	29.8	9	6	US-10-538-066-644	Sequence 644, App
88	17	29.8	9	7	US-11-140-487A-583	Sequence 583, App
89	17	29.8	9	7	US-11-140-487A-1157	Sequence 1157, Ap
90	17	29.8	9	7	US-11-140-487A-1237	Sequence 1237, Ap
91	17	29.8	9	7	US-11-023-959A-24	Sequence 24, Appl
92	17	29.8	9	7	US-11-338-842-4	Sequence 4, Appl
93	17	29.8	9	7	US-11-340-431-55	Sequence 55, Appl
94	17	29.8	9	7	US-11-340-431-162	Sequence 162, App
95	17	29.8	9	7	US-11-099-283B-179	Sequence 179, App
96	17	29.8	9	7	US-11-099-283B-185	Sequence 185, App
97	17	29.8	9	7	US-11-099-283B-193	Sequence 190, App
98	17	29.8	9	7	US-11-099-283B-263	Sequence 263, App

99 17 29.8 10 6 US-10-538-066-633 Sequence 633, App  
100 17 29.8 10 6 US-10-449-902-35223 Sequence 35223, A

## ALIGNMENTS

RESULT 1  
US-11-214-588-1  
; Sequence 1, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Decapeptide derived from Homo sapiens G-alpha-i3  
US-11-214-588-1

Query Match 100.0%; Score 57; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKECGLY 10  
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Db 1 KNNLKECGLY 10

RESULT 2  
US-11-214-588-3  
; Sequence 3, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; NAME/KEY: BINDING  
; LOCATION: (1)-(10)  
; OTHER INFORMATION: A bond exists between the side chain of K at position 1 and the  
; OTHER INFORMATION: c-terminus of the peptide  
US-11-214-588-3

Query Match 100.0%; Score 57; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0001;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNNLKECGLY 10  
| | | | | | | | | |  
Db 1 KNNLKECGLY 10

RESULT 3  
US-11-214-588-4  
; Sequence 4, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; NAME/KEY: MISC FEATURE  
; LOCATION: (10)-(10)  
; OTHER INFORMATION: Para-amino Phenylalanine at position 10  
US-11-214-588-4

Query Match 93.0%; Score 53; DB 7; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.00055;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKECGLY 10  
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Db 1 KNNLKECGLF 10

RESULT 4  
US-11-214-588-6  
; Sequence 6, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-214-588-6

Query Match 91.2%; Score 52; DB 7; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.00084;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:58:13 ; Search time 13.5 Seconds  
(without alignments)  
71.272 Million cell updates/sec

Title: US-10-009-809-1  
Perfect score: 57  
Sequence: 1 KNNLKEGGLY 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	38.6	5	2 S65726	hemoglobin, extrac
2	22	38.6	7	2 A11483	aspartate transami
3	20	35.1	5	2 A33882	cadmium-binding pe
4	20	35.1	7	2 B33882	cadmium-binding he
5	20	35.1	7	2 C56793	platelet glycoprot
6	18	31.6	10	2 A47593	mercury resistance
7	17	29.8	7	2 A58512	venom heptapeptide
8	16	28.1	10	2 A35556	hypothetical prote
9	15.5	27.2	10	2 S51912	hemagglutinin - in
10	15	26.3	4	2 S55238	pallidipin - aasas
11	15	26.3	6	4 I79564	hypothetical rcl3
12	15	26.3	8	2 A21440	variant surface gl
13	15	26.3	9	4 I73804	hypothetical E2 pr
14	15	26.3	10	1 ECLQ3M	tachykinin III - m
15	15	26.3	10	2 E49033	T-cell receptor ga
16	15	26.3	10	2 F49033	T-cell receptor ga
17	14	24.6	5	2 B45525	actin I - malaria
18	14	24.6	6	2 JN0861	peptidyl-di-peptida
19	14	24.6	6	2 I67345	MHC H2-K-k cell su
20	14	24.6	7	2 S45648	Na+-transporting A
21	14	24.6	8	2 A14683	aspartate transami
22	14	24.6	9	2 A93408	oxytocin - Austral
23	14	24.6	9	2 A92774	oxytocin - spotted
24	14	24.6	9	2 A93147	oxytocin - finback
25	14	24.6	9	2 A91466	oxytocin - hippopo
26	14	24.6	9	2 B90667	oxytocin - rabbit
27	14	24.6	10	2 S65728	hemoglobin, extrac
28	14	24.6	10	2 H61308	hemocyanin subunit
29	14	24.6	10	2 PH0933	T-cell receptor be

30	14	24.6	10	2 S27873	hypothetical prote
31	13	22.8	6	2 T11779	phosphoglycerate t
32	13	22.8	6	2 I49424	cytotoxic T-lympho
33	13	22.8	8	2 S70727	ip9F protein - Shi
34	13	22.8	8	2 FA0032	protein QA300040 -
35	13	22.8	8	2 S19288	acylase - Kluyvera
36	13	22.8	8	2 C61512	variant surface gl
37	13	22.8	9	2 A28495	conopressin G - co
38	13	22.8	9	2 B28495	conopressin S - co
39	13	22.8	9	2 E28854	fibrinopeptide B -
40	13	22.8	9	2 F28854	fibrinopeptide B -
41	13	22.8	9	2 D28854	fibrinopeptide B -
42	13	22.8	9	2 S66608	quinoline 2-oxidor
43	13	22.8	9	2 S39040	lysine-conopressin
44	13	22.8	10	1 ECLQ1M	tachykinin I - mig
45	13	22.8	10	2 S70722	65.4K GTP-binding
46	13	22.8	10	2 S70251	nitrogenase (EC 1.
47	13	22.8	10	2 C54226	light-harvesting p
48	12	21.1	5	2 A32014	tram protein - Esc
49	12	21.1	6	2 F41946	T-cell receptor ga
50	12	21.1	7	2 S78024	ribosomal protein
51	12	21.1	7	2 A34026	acetylcholinestera
52	12	21.1	7	2 S33244	neuromodulatory pe
53	12	21.1	7	2 S08606	hypothetical prote
54	12	21.1	8	2 PT0627	T-cell receptor be
55	12	21.1	8	2 A25836	L-serine ammonia-1
56	12	21.1	9	2 PH0942	T-cell receptor be
57	12	21.1	9	2 S02384	probable membrane
58	12	21.1	9	2 JP0073	ribosomal protein
59	12	21.1	9	2 FC2021	oxytocin-related p
60	12	21.1	9	2 S06375	arginine vasotocin
61	12	21.1	9	2 B61364	vasotocin - common
62	12	21.1	9	2 I46016	cytokerin 4 - bo
63	12	21.1	10	2 A61131	hydrin 2 - bullfro
64	12	21.1	10	2 S42282	parapapal crystal
65	12	21.1	10	2 S62208	polyferredoxin - M
66	12	21.1	10	2 PT0243	Ig heavy chain CRD
67	12	21.1	10	2 S23370	T-cell receptor al
68	12	21.1	10	2 B24736	inhibin beta-8 cha
69	12	21.1	10	2 PH0807	T-cell receptor al
70	12	21.1	10	2 E41946	T-cell receptor ga
71	12	21.1	10	2 C41946	T-cell receptor ga
72	12	21.1	10	2 S65385	cytochrome-c oxida
73	12	21.1	10	2 A39745	endo-glucosylceram
74	12	21.1	10	2 S30348	clotting protein -
75	12	21.1	10	2 S43631	cytochrome-c oxida
76	12	21.1	10	2 G60527	sperm-activating p
77	12	21.1	10	2 F60589	sperm-activating p
78	11	19.3	5	2 PQ0009	angiotensin-conver
79	11	19.3	6	2 I65546	MHC H2-L antigen -
80	11	19.3	6	2 PT0652	T-cell receptor be
81	11	19.3	7	2 S58797	serine/threonine-s
82	11	19.3	8	2 S59622	metallothionein is
83	11	19.3	8	2 A39892	P element, P cytot
84	11	19.3	8	2 PN0043	phosphatidylethano
85	11	19.3	8	2 A61597	cytochrome P450 AL
86	11	19.3	8	2 I57532	gene Tnslow prote
87	11	19.3	8	2 S66646	cardioacceleratory
88	11	19.3	9	2 A61364	isotocin - common
89	11	19.3	9	2 A48873	caldesmon - rabbit
90	11	19.3	9	2 A61230	caldesmon - car
91	11	19.3	9	2 PT0272	Ig heavy chain CRD
92	11	19.3	9	2 G56978	collagen alpha 1(I
93	11	19.3	9	2 S36850	Tg heavy chain v r
94	11	19.3	9	2 G41946	T-cell receptor ga
95	11	19.3	9	2 S39767	cardioactive pepti
96	11	19.3	9	2 S55696	phosphoenolpyruvat
97	11	19.3	9	2 A26363	cardioactive pepti
98	11	19.3	9	2 S27233	cardioactive pepti
99	11	19.3	9	2 JQ1202	leader peptide - p
100	11	19.3	9	2 S19329	sperm-activating p

## ALIGNMENTS

RESULT 1  
S65726  
hemoglobin, extracellular, chain b - earthworm (Lumbricus terrestris) (fragment)  
C;Species: Lumbricus terrestris (common earthworm)  
C;Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C;Accession: S65726  
R;Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.  
Biochim. Biophys. Acta 1292, 273-280, 1996  
A;Title: Characterization of the constituent polypeptides of the extracellular hemoglobin  
A;Reference number: S65721; MUID:96176855; PMID:8597573  
A;Accession: S65726  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <FUS>  
A;Cross-references: UNIPARC:UPI0000017BD81

Query Match 38.6%; Score 22; DB 2; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KECG 8  
|:|  
Db 2 KQCG 5

RESULT 2  
A11483  
aspartate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)  
N;Alternate names: aspartate aminotransferase, mitochondrial  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 20-Aug-1999  
C;Accession: A11483  
R;Campos-Cavieles, M.; Milstein, C.P.  
Biochem. J. 147, 275-281, 1975  
A;Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mitochondrial  
A;Reference number: A11483; MUID:76039441; PMID:1180894  
A;Accession: A11483  
A;Molecule type: protein  
A;Residues: 1-7 <CAM>  
A;Cross-references: UNIPARC:UPI0000017C59C  
A;Experimental source: liver  
C;Keywords: aminotransferase; mitochondrial; phosphoprotein; pyridoxal phosphate  
F;2/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 38.6%; Score 22; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KECGLY 10  
|:|  
Db 2 KBMGly 7

RESULT 3  
A33882  
cadmium-binding pentapeptide - downy thornapple  
C;Species: Datura innoxia (downy thornapple)  
C;Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 18-Jun-1993  
C;Accession: A33882  
R;Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987  
A;Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant  
A;Reference number: A94182; MUID:88016144; PMID:3477793  
A;Accession: A33882  
A;Molecule type: protein  
A;Residues: 1-5 <JAC>  
A;Cross-references: UNIPARC:UPI0000017B088

Query Match 35.1%; Score 20; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ECG 8  
|:|  
Db 3 ECG 5

RESULT 4  
B33882  
cadmium-binding heptapeptide - downy thornapple  
C;Species: Datura innoxia (downy thornapple)  
C;Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 18-Jun-1993  
C;Accession: B33882  
R;Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987  
A;Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant  
A;Reference number: A94182; MUID:88016144; PMID:3477793  
A;Accession: B33882  
A;Molecule type: protein  
A;Residues: 1-7 <JAC>  
A;Cross-references: UNIPARC:UPI0000017B087

Query Match 35.1%; Score 20; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ECG 8  
|:|  
Db 5 ECG 7

RESULT 5  
C56793  
platelet glycoprotein GPIIa - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 07-Feb-1997  
C;Accession: C56793  
R;Catmel, B.; Farmentier, S.; Leung, L.L.; McGregor, J.L.  
Biochem. J. 279, 419-425, 1991  
A;Title: Separation of important new platelet glycoproteins (GPIa, GPIC, GPIc\*, GPIIa and  
A;Reference number: A56793; MUID:92061944; PMID:1953640  
A;Accession: C56793  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <CAT>  
A;Cross-references: UNIPARC:UPI0000017C2F5  
A;Experimental source: platelet  
C;Keywords: glycoprotein

Query Match 35.1%; Score 20; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 NLKECG 8  
|:|  
Db 2 NLDEAG 7

RESULT 6  
A47593  
mercury resistance regulatory protein merR - Pseudomonas aeruginosa transposon Tn501 (fr  
C;Species: Pseudomonas aeruginosa  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Aug-1998  
C;Accession: A47593  
R;O'Halloran, T.; Walsh, C.  
Science 235, 211-214, 1987  
A;Title: Metalloregulatory DNA-binding protein encoded by the merR gene: isolation and  
A;Reference number: A47593; MUID:87094195; PMID:3798107  
A;Accession: A47593  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <OAH>  
A;Cross-references: UNIPARC:UPI000001787DE

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:57:41 ; Search time 80.5 Seconds  
(without alignments)  
114.909 Million cell updates/sec

Title: US-10-009-809-1

Perfect score: 57

Sequence: 1 KNNKECGLY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 3727

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt\_7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	45.6	10	2	Q71VN2_MOUSE
2	24	42.1	10	2	Q48469_KLEPN
3	21	36.8	8	2	Q9AGP4_9MICC
4	20	35.1	7	2	Q9C5B3_ARATH
5	20	35.1	9	2	Q5J2D2_ASPAW
6	20	35.1	9	2	Q38340_9CAUD
7	20	35.1	10	1	SYK_CAMUP
8	20	35.1	10	2	Q8NEY9_HUMAN
9	18	31.6	9	2	Q6T3B6_CHLRE
10	18	31.6	10	1	QWPI4_LYCES
11	18	31.6	10	2	Q7RQJ0_PLAYO
12	18	31.6	10	2	Q71HU9_ICTSP
13	17	29.8	7	1	ASCL_ALLAS
14	17	29.8	7	1	BRHP_CONIM
15	17	29.8	7	2	Q551B4_RAT
16	17	29.8	9	2	Q7RDA8_PLAYO
17	17	29.8	10	1	SC43_TITCA
18	17	29.8	10	2	Q4YFMS_PLABE
19	17	29.8	10	2	Q60194_9MOLU
20	17	29.8	10	2	Q64G36_9CORA
21	16	28.1	8	2	Q6EGT1_9PLEO
22	16	28.1	8	2	Q6EGV0_9PLEO
23	16	28.1	8	2	Q6EGV3_9PLEO
24	16	28.1	8	2	Q6EGW2_9PLEO
25	16	28.1	9	2	Q7XB03_MAIZE
26	16	28.1	9	2	Q7R8X5_PLAYO
27	16	28.1	9	2	Q562A7_ARATH
28	16	28.1	9	2	Q7X8P7_MAIZE
29	16	28.1	9	2	Q8RKU3_BORBU
30	16	28.1	10	2	Q7RZZ2_NEUCR
31	16	28.1	10	2	P82937_HORVU

32	16	28.1	10	2	Q68SM8_CHAPN
33	16	28.1	10	2	Q68SM9_THOMO
34	16	28.1	10	2	Q68SN0_CRATY
35	16	28.1	10	2	Q68SN1_CRAGY
36	16	28.1	10	2	Q73589_CHICK
37	15	26.3	7	2	Q8GL04_BORBU
38	15	26.3	7	2	Q8GL12_BORBU
39	15	26.3	7	2	Q8J20_CHICK
40	15	26.3	8	2	Q71UR9_HUMAN
41	15	26.3	8	2	Q79B39_BORGA
42	15	26.3	8	2	Q7X4C1_9MOLU
43	15	26.3	8	2	Q8G940_BORBU
44	15	26.3	8	2	Q8GL21_BORBU
45	15	26.3	8	2	Q98TUS_XENLA
46	15	26.3	9	2	Q31363_BORGA
47	15	26.3	9	2	Q8GL26_BORBU
48	15	26.3	9	2	Q9R3T0_BORAF
49	15	26.3	9	2	Q9R792_BORBU
50	15	26.3	9	2	Q8GL31_BORBU
51	15	26.3	9	2	Q9R9C4_BORBU
52	15	26.3	9	2	Q12096_CAEV
53	15	26.3	9	2	Q12098_CAEV
54	15	26.3	9	2	Q12100_CAEV
55	15	26.3	9	2	Q12102_CAEV
56	15	26.3	9	2	Q12104_CAEV
57	15	26.3	10	1	AMPN_HELAM
58	15	26.3	10	1	MBSP_SAUWA
59	15	26.3	10	1	TKLA_LOCHI
60	15	26.3	10	2	Q7R926_PLAYO
61	15	26.3	10	2	Q8SPN8_MACMU
62	15	26.3	10	2	Q8WP04_ATEBE
63	15	26.3	10	2	Q60192_SPIKU
64	15	26.3	10	2	Q83YL7_ACILW
65	15	26.3	10	2	Q9FSW1_VIBCH
66	15	26.3	10	2	Q9R791_BORAF
67	15	26.3	10	2	Q8G8W5_BORBU
68	15	26.3	10	2	Q5UCC2_MOUSE
69	15	26.3	10	2	Q8CJ31_MOUSE
70	15	26.3	10	2	Q6M69_9VIRU
71	15	26.3	10	2	Q718N9_9PARA
72	14	24.6	8	1	FAR2_MACRS
73	14	24.6	8	2	Q6LDP0_HUMAN
74	14	24.6	8	2	Q40659_ORYSA
75	14	24.6	8	2	Q6D021_CLOBE
76	14	24.6	8	2	Q7LZ21_CHICK
77	14	24.6	9	1	QWP07_LYCES
78	14	24.6	9	1	FAR3_MACRS
79	14	24.6	9	1	NEUL_BALPH
80	14	24.6	9	1	NEUL_HIPAM
81	14	24.6	9	1	NEUL_RABIT
82	14	24.6	9	1	NEUL_TACAC
83	14	24.6	9	1	OXYT_HYDCO
84	14	24.6	9	2	Q2QZAB_CAEEL
85	14	24.6	9	2	Q43928_AERPU
86	14	24.6	9	2	Q44001_9GAMM
87	14	24.6	9	2	Q44377_AERTR
88	14	24.6	9	2	Q44468_9GAMM
89	14	24.6	9	2	Q57328_AERHO
90	14	24.6	9	2	Q6LAR8_AERHY
91	14	24.6	10	1	SCP15_LYCES
92	14	24.6	10	1	SCP37_TITCA
93	14	24.6	10	2	Q8NGB1_HUMAN
94	14	24.6	10	2	Q75MD5_HUMAN
95	14	24.6	10	2	Q67B26_9CAUD
96	14	24.6	10	2	Q50032_MYCLE
97	14	24.6	10	2	Q9JN49_STAAU
98	14	24.6	10	2	Q9RSN4_CLOBO
99	14	24.6	10	2	Q61807_MOUSE
100	14	24.6	10	2	Q2L587_HBV

ALIGNMENTS

```
RESULT 1
Q71VN2_MOUSE PRELIMINARY; PRT; 10 AA.
AC Q71VN2_MOUSE PRELIMINARY; PRT; 10 AA.
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 9.
DE Secretory leukoprotease inhibitor (Fragment).
GN Names=Slpi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129SV;
RX MEDLINE=99061820; PubMed=9843921;
RA Kikuchi T., Abe T., Hoshi S., Matsubara N., Tominaga Y., Satoh K.,
RA Nukiwa T.;
RT "Structure of the murine secretory leukoprotease inhibitor (Slpi) gene
RL Am. J. Respir. Cell Mol. Biol. 19:875-880(1998).
CC -----
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CC -----
DR EMBL; AF002720; AAD09308.1; -; Genomic_DNA.
DR MGI; MGI:109297; Slpi.
DR GO; GO:0005615; C:extracellular space; RCA.
KW Protease.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1096 MW; 8651EE6727287EA5 CRC64;

Query Match 45.6%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 8.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LKECGL 9
DB 1 MKSCGL 6

RESULT 2
Q48469_KLEPN PRELIMINARY; PRT; 10 AA.
AC Q48469_KLEPN PRELIMINARY; PRT; 10 AA.
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DE 07-FEB-2006, entry version 15.
DE Nitrogenase (Fragment).
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83246546; PubMed=6306580;
RA Shen S., Xue Z., Kong Q., Wu Q.;
RT "An open reading frame upstream from the nifH gene of Klebsiella
RL Nucleic Acids Res. 11:4241-4250(1983).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; X01006; CAA25501.1; -; Genomic_DNA.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1173 MW; B130695DDEA6C406 CRC64;

Query Match 42.1%; Score 24; DB 2; Length 10;
Best Local Similarity 28.6%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 4 LKECGL 9
DB 1 MKSCGL 6

RESULT 4
Q9C5B3_ARATH PRELIMINARY; PRT; 7 AA.
AC Q9C5B3_ARATH PRELIMINARY; PRT; 7 AA.
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DE 07-FEB-2006, entry version 13.
DE Hypothetical protein DiDi 10A-2b (Fragment).
GN Names=DiDi 10A-2b;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Roots;
RX MEDLINE=21171025; PubMed=11277426;
RA Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
RT "Arabidopsis thaliana genes expressed in the early compatible
RT interaction with root-knot nematodes.";
RL Mol. Plant Microbe Interact. 14:288-295(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Roots;
RA Vercauteren I., J.R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -----

Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 LKECGL 10
DB 3 MRQCAIY 9

RESULT 3
Q9AGP4_9MICC PRELIMINARY; PRT; 8 AA.
AC Q9AGP4_9MICC PRELIMINARY; PRT; 8 AA.
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE Serine hydroxymethyltransferase (Fragment).
GN Name=glyA;
OS Arabidopsis thaliana.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=153502;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LIN;
RA Meskys R., Harris R.J., Casate V., Basran J., Scrutton N.S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF329478; AAK16486.1; -; Genomic_DNA.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Methyltransferase; Transferase.
FT NON TER 1 1
SQ SEQUENCE 8 AA; 898 MW; 6B1870533372457 CRC64;

Query Match 36.8%; Score 21; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NLKECG 8
DB 2 NLKKIG 7

RESULT 4
Q9C5B3_ARATH PRELIMINARY; PRT; 7 AA.
AC Q9C5B3_ARATH PRELIMINARY; PRT; 7 AA.
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DE 07-FEB-2006, entry version 13.
DE Hypothetical protein DiDi 10A-2b (Fragment).
GN Names=DiDi 10A-2b;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Roots;
RX MEDLINE=21171025; PubMed=11277426;
RA Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
RT "Arabidopsis thaliana genes expressed in the early compatible
RT interaction with root-knot nematodes.";
RL Mol. Plant Microbe Interact. 14:288-295(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Roots;
RA Vercauteren I., J.R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -----
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:55:58 ; Search time 58 Seconds  
(without alignments)  
78.830 Million cell updates/sec

Title: US-10-009-809-2  
Perfect score: 57  
Sequence: 1 KNNLKDGLF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 606527

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A Geneseq\_8.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*
- 10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	57	100.0	10	2	AAR61259 Control p
2	57	100.0	10	2	AAR49785 Farnesylt
3	57	100.0	10	2	AAR04476 Weak inh
4	57	100.0	10	5	AAR26151 Galphai2
5	51	89.5	10	1	AAP82558 Guanin d
6	51	89.5	10	1	AAP82558 Guanin d
7	50	87.7	10	5	AAR26130 Galphai3
8	50	87.7	10	5	AAR26131 Galphai3
9	47	82.5	10	5	AAR26129 Galphai3
10	45	78.9	10	5	AAR26132 Anti-alle
11	44	77.2	10	5	AAR26134 Anti-alle
12	44	77.2	10	5	AAR26133 Anti-alle
13	40	70.2	10	5	AAR26136 Anti-alle
14	40	70.2	7	7	ABW00034 Human G a
15	40	70.2	10	5	AAR26135 Anti-alle
16	39	68.4	10	1	AAP82561 Peptide d
17	31	54.4	5	3	AAY79272 Guanine n
18	31	54.4	5	4	AAU04390 Human G-P
19	31	54.4	5	5	ABJ77869 Amino aci
20	31	54.4	5	5	ABJ04080 Human G p
21	31	54.4	5	5	ABG95176 GPCR Galp
22	31	54.4	5	6	ABR44440 Human G p
23	31	54.4	5	6	AAO26778 Galphas C

24	31	54.4	5	6	ABU13802	Abu13802 Modified
25	31	54.4	5	6	ABR62603	AbR62603 G protein
26	31	54.4	5	7	ADL96577	ADL96577 G protein
27	31	54.4	5	8	ADN11612	ADN11612 Human G p
28	31	54.4	5	8	ADP04975	ADP04975 Human HM7
29	31	54.4	5	8	ADS64576	ADS64576 G protein
30	31	54.4	5	8	ADW373821	ADW373821 Mouse Gal
31	31	54.4	5	9	ADM44750	ADM44750 Gq (del)/
32	31	54.4	5	9	ADM11145	ADM11145 Mouse Gia
33	31	54.4	5	9	ADZ88295	ADZ88295 Chimeric
34	31	54.4	5	9	AEB20934	AEb20934 G-alpha-i
35	31	54.4	5	10	AEET75308	Aee75308 Rat Galph
36	31	54.4	5	10	AEET75308	Aee75308 LPSR1 ass
37	31	54.4	5	7	ADE68698	Ade68698 Human 161
38	31	54.4	9	7	ADE67532	Ade67532 Human 161
39	31	54.4	9	7	ADE69088	Ade69088 Human 161
40	31	54.4	9	7	ADE68274	Ade68274 Human 161
41	31	54.4	10	7	ADE66418	Ade66418 Human 161
42	31	54.4	10	7	ADE69278	Ade69278 Human 161
43	29	50.9	9	9	AEC97844	Aec97844 HLA-A24-b
44	29	50.9	10	5	ABB51637	Abb51637 Human 34P
45	29	50.9	10	5	ADV25849	Adv25849 SARS coro
46	28	49.1	10	2	AAy47548	Aay47548 Immunogen
47	28	49.1	10	6	ABJ19587	Abj19587 Neuronal
48	28	49.1	10	6	ABJ19551	Abj19551 Neuronal
49	27	47.4	5	3	AAy79273	Aay79273 G alpha p
50	27	47.4	5	6	ABU13803	Abu13803 Modified
51	27	47.4	8	10	AEF05892	Aef05892 Human AFP
52	27	47.4	9	5	ABB51855	Abb51855 Human 34P
53	27	47.4	9	5	ABB51663	Abb51663 Human 34P
54	27	47.4	9	5	ABB51554	Abb51554 Human 34P
55	27	47.4	9	5	ABB51754	Abb51754 Human 34P
56	27	47.4	9	5	ABB51351	Abb51351 Human 34P
57	27	47.4	9	5	ABB51552	Abb51552 Human 34P
58	27	47.4	9	5	ABB51475	Abb51475 Human 34P
59	27	47.4	9	5	ABB51773	Abb51773 Human 34P
60	27	47.4	9	9	AEC33159	Aec33159 APP tumor
61	27	47.4	10	3	AAb27133	Aab27133 Human CAS
62	27	47.4	10	5	AAU78994	Aau78994 Histone H
63	27	47.4	10	5	ABB51397	Abb51397 Human 34P
64	27	47.4	10	5	ABB51500	Abb51500 Human 34P
65	27	47.4	10	5	ABB51288	Abb51288 Human 34P
66	27	47.4	10	5	ABB51496	Abb51496 Human 34P
67	27	47.4	10	5	ABB51689	Abb51689 Human 34P
68	27	47.4	10	6	ADa13507	Ada13507 Human H4
69	27	47.4	10	9	ADY34403	Ady34403 Modified
70	26	45.6	7	8	ADN08485	Adn08485 Cotton te
71	26	45.6	8	7	ABU62826	Abu62826 Human LTB
72	26	45.6	9	4	AAm98674	Aam98674 Human pep
73	26	45.6	9	7	ADC44797	Adc44797 Endotheli
74	26	45.6	9	8	ADN67888	Adn67888 Human 273
75	26	45.6	9	8	ADN69294	Adn69294 Human 273
76	26	45.6	9	8	ADN66092	Adn66092 Human 273
77	26	45.6	9	8	ADN67026	Adn67026 Human 273
78	26	45.6	9	8	ADN68445	Adn68445 Human 273
79	26	45.6	9	8	ADN68871	Adn68871 Human 273
80	26	45.6	9	8	ADN66899	Adn66899 Human 273
81	26	45.6	9	8	ADN69516	Adn69516 Human 273
82	26	45.6	10	5	AAU70200	Aau70200 HIV gp41
83	26	45.6	10	8	ADL71998	Adl71998 Glypican-
84	26	45.6	10	8	ADN69944	Adn69944 Human 273
85	26	45.6	10	8	ADN69733	Adn69733 Human 273
86	26	45.6	10	8	ADN69991	Adn69991 Human 273
87	26	45.6	10	8	ADN70462	Adn70462 Human 273
88	25	43.9	6	6	ABP56238	Abp56238 Targeting
89	25	43.9	6	8	ADH564329	Adh564329 Radiophar
90	25	43.9	6	8	ADH58573	Adh58573 Radiophar
91	25	43.9	6	8	ADQ76938	Adq76938 Maize/ric
92	25	43.9	6	8	ADQ76957	Adq76957 Maize/oat
93	25	43.9	6	9	AEC31520	Aec31520 Peptide o
94	25	43.9	6	9	AEB64946	Aeb64946 Radiophar
95	25	43.9	6	10	AEF82962	Aef82962 ADAMI2 lo
96	25	43.9	9	3	AAy69189	Aay69189 Peptide u

97 25 43.9 9 4 AAB76057 Trypanoso  
98 25 43.9 9 5 AAU78890 Endotheli  
99 25 43.9 9 7 ADE68328 Human 161  
100 25 43.9 9 7 ADE66562 Human 161

## ALIGNMENTS

## RESULT 1

AAR61259  
ID AAR61259 standard; peptide; 10 AA.

XX AC AAR61259;  
XX

XX 25-MAR-2003 (revised)  
DT

XX 13-APR-1995 (first entry)  
DT

XX Control peptide corresponding to Gi2 alpha Lys346-Phe355.  
DE

XX Anticouplone; G-protein; Regulator region; Immunosuppressant.  
KW

XX Synthetic.  
OS

XX WO9419002-A1.  
PN

XX 01-SEP-1994.  
PD

XX 17-FEB-1994; 94WO-US001768.  
PF

XX 18-FEB-1993; 93US-00019073.  
PR

XX (GEHO ) GEN HOSPITAL CORP.  
PA

XX Nishimoto I;  
PI

XX WPI; 1994-293996/36.  
DR

XX Anticouplone sequences of G proteins - inhibit activation of G protein by  
PT G-coupled receptor, used to treat neuromuscular and autoimmune diseases,  
PT cancer, diabetes, hypertension, AIDS etc.  
XX

XX Disclosure; Page 8; 52pp; English.  
PS

XX Control peptide, showed no effect on peptide (AAR61267) induced Gi2  
CC activation. (Updated on 25-MAR-2003 to correct PN field.)  
CC

XX Sequence 10 AA;  
SQ

Query Match 100.0%; Score 57; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10  
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Db 1 KNNLKDCGLF 10  
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## RESULT 2

AAR49785  
ID AAR49785 standard; peptide; 10 AA.

XX AC AAR49785;  
XX

XX 25-MAR-2003 (revised)  
DT

XX 08-AUG-1994 (first entry)  
DT

XX Farnesyltransferase-inhibitor.  
DE

XX Farnesyltransferase-inhibitor; farnesyltransferase; FT; p21ras;  
KW ras protein; farnesylation; cancer therapy.

XX Synthetic.  
OS

XX WO9404561-A1.  
PN

XX 03-MAR-1994.  
PD

XX 24-AUG-1993; 93WO-US008062.  
PF

XX 24-AUG-1992; 92US-00935087.  
PR

XX (TEXA ) UNIV TEXAS SYSTEM.  
PA

XX (GETH ) GENENTECH INC.  
PA

XX Brown MS, Goldstein JL, Reiss Y, Marsters JC;  
PI

XX WPI; 1994-083105/10.  
DR

XX New farnesyl-transferase inhibitors - used for inhibiting attachment of a  
PT farnesyl moiety to a p21ras protein in malignant cells.

XX Disclosure; Page 49; 183pp; English.  
PS

XX Peptides given in AAR49741-75, AAR49777-78 and AAR49785-88, which include  
CC a family of tetrapeptides based on the recognition site (AAR49776) of  
CC farnesyltransferase (FT), are potential anticancer agents that inhibit  
CC FT, thereby preventing expression of p21ras. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
CC

XX Sequence 10 AA;  
SQ

Query Match 100.0%; Score 57; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10  
|||||

Db 1 KNNLKDCGLF 10  
|||||

## RESULT 3

AAW04476  
ID AAW04476 standard; peptide; 10 AA.

XX AC AAW04476;  
XX

XX 05-AUG-1997 (first entry)  
DT

XX Weak inhibitor of farnesyl transferase.  
DE

XX Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;  
KW ras protein; K-ras B; malignant; detection; identification.  
XX

XX Synthetic.  
OS

XX WO9634113-A2.  
PN

XX 31-OCT-1996.  
PD

XX 29-APR-1996; 96WO-US005969.  
PF

XX 27-APR-1995; 95US-00429964.  
PR

XX (TEXA ) UNIV TEXAS SYSTEM.  
PA

XX Brown MS, Goldstein JL, James GL;  
PI

XX WPI; 1996-497642/49.  
DR

XX Assay for farnesyl transferase activity - by determining ability to  
PT transfer farnesyl moiety to K-Ras B protein, partic. useful for  
PT identifying inhibitors.  
PT

XX Disclosure; Page 179; 257pp; English.  
PS



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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:59:01 ; Search time 21 Seconds  
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41.681 Million cell updates/sec

Title: US-10-009-809-2

Perfect score: 57

Sequence: 1 KNNLKDCGLF 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 176806

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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7: /EMC Celerra\_SID83/prodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	57	100.0	10	1	US-08-429-964-50
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4	57	100.0	10	5	PCT-US94-01768-19
5	57	100.0	10	7	5428134-6
6	57	100.0	10	7	5428134-6
7	51	89.5	10	7	5428134-1
8	51	89.5	10	7	5428134-10
9	51	89.5	10	7	5436320-1
10	51	89.5	10	7	5436320-7
11	39	68.4	10	7	5428134-4
12	39	68.4	10	7	5436320-4
13	31	54.4	5	2	US-10-314-048A-131
14	29	50.9	8	3	US-09-641-528B-6112
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16	29	50.9	8	3	US-09-641-528B-14504
17	29	50.9	8	3	US-09-641-528B-14511
18	29	50.9	8	3	US-09-641-528B-27731
19	29	50.9	8	3	US-09-641-528B-27736
20	29	50.9	9	3	US-09-641-528B-6120
21	29	50.9	9	3	US-09-641-528B-14512
22	29	50.9	9	3	US-09-641-528B-19092
23	29	50.9	9	3	US-09-641-528B-27737
24	29	50.9	9	3	US-09-641-528B-49574
25	29	50.9	9	3	US-09-641-528B-51040
26	29	50.9	10	3	US-09-641-528B-6217

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28	50.9	10	3	US-09-641-528B-19093	Sequence 19093, A
29	50.9	10	3	US-09-641-528B-22573	Sequence 22573, A
30	50.9	10	3	US-09-641-528B-35962	Sequence 35962, A
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33	49.1	8	3	US-09-641-528B-42759	Sequence 42759, A
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35	49.1	8	3	US-09-641-528B-42760	Sequence 42760, A
36	49.1	10	3	US-09-641-528B-35970	Sequence 35970, A
37	49.1	10	3	US-09-641-528B-42761	Sequence 42761, A
38	47.4	8	3	US-09-641-528B-4739	Sequence 4739, Ap
39	47.4	8	3	US-09-641-528B-4747	Sequence 4747, Ap
40	47.4	8	3	US-09-641-528B-13579	Sequence 13579, A
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43	47.4	9	3	US-09-641-528B-13585	Sequence 13585, A
44	47.4	9	3	US-09-641-528B-26652	Sequence 26652, A
45	47.4	9	3	US-09-641-528B-49190	Sequence 49190, A
46	47.4	9	3	US-09-641-528B-50983	Sequence 50983, A
47	47.4	10	3	US-09-641-528B-4843	Sequence 4843, Ap
48	47.4	10	3	US-09-641-528B-10151	Sequence 10151, A
49	47.4	10	3	US-09-641-528B-18682	Sequence 18682, A
50	47.4	10	3	US-09-641-528B-34443	Sequence 34443, A
51	47.4	10	3	US-09-641-528B-41760	Sequence 41760, A
52	45.6	7	1	US-08-467-587A-32	Sequence 32, Appl
53	45.6	8	3	US-09-641-528B-34450	Sequence 34450, A
54	45.6	8	3	US-09-641-528B-41766	Sequence 41766, A
55	45.6	9	3	US-09-641-528B-34451	Sequence 34451, A
56	45.6	9	3	US-09-641-528B-41767	Sequence 41767, A
57	45.6	10	3	US-09-641-528B-34452	Sequence 34452, A
58	45.6	10	3	US-09-641-528B-41768	Sequence 41768, A
59	44.7	9	2	US-08-678-735A-10	Sequence 10, Appl
60	44.7	9	2	US-08-418-992-10	Sequence 10, Appl
61	43.9	6	2	US-10-131-346-3	Sequence 3, Appl
62	43.9	6	2	US-10-131-546-3	Sequence 3, Appl
63	43.9	6	2	US-10-131-546-3	Sequence 3, Appl
64	43.9	8	2	US-08-981-392-90	Sequence 90, Appl
65	43.9	8	2	US-09-908-322-90	Sequence 90, Appl
66	43.9	8	3	US-09-641-528B-7645	Sequence 7645, Ap
67	43.9	8	3	US-09-641-528B-15566	Sequence 15566, A
68	43.9	8	3	US-09-641-528B-28985	Sequence 28985, A
69	43.9	9	2	US-08-592-500-5	Sequence 5, Appl
70	43.9	9	2	US-08-195-006-5	Sequence 5, Appl
71	43.9	9	2	US-09-775-803-10	Sequence 10, Appl
72	43.9	9	2	US-09-641-528B-15443	Sequence 15443, A
73	43.9	9	3	US-09-641-528B-19499	Sequence 19499, A
74	43.9	9	3	US-09-641-528B-48916	Sequence 48916, A
75	43.9	9	3	US-09-641-528B-49949	Sequence 49949, A
76	43.9	9	3	US-09-641-528B-50006	Sequence 50006, A
77	43.9	9	3	US-09-641-528B-51105	Sequence 51105, A
78	43.9	9	5	PCT-US94-0764A-5	Sequence 5, Appl
79	43.9	10	1	US-08-687-916-5	Sequence 5, Appl
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82	43.9	10	3	US-09-641-528B-10961	Sequence 10961, A
83	43.9	10	3	US-09-641-528B-19500	Sequence 19500, A
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85	43.9	10	3	US-09-641-528B-37639	Sequence 37639, A
86	43.9	10	3	US-09-641-528B-43810	Sequence 43810, A
87	42.1	8	3	US-09-641-528B-3634	Sequence 3634, Ap
88	42.1	8	3	US-09-641-528B-12792	Sequence 12792, A
89	42.1	8	3	US-09-641-528B-18259	Sequence 18259, A
90	42.1	8	3	US-09-641-528B-19498	Sequence 19498, A
91	42.1	8	3	US-09-641-528B-25694	Sequence 25694, A
92	42.1	8	7	5310729-20	Patent No. 5310729
93	42.1	9	3	US-09-641-528B-3530	Sequence 3530, Ap
94	42.1	9	3	US-09-641-528B-7541	Sequence 7541, Ap
95	42.1	9	3	US-09-641-528B-12655	Sequence 12655, A
96	42.1	9	3	US-09-641-528B-21089	Sequence 21089, A
97	42.1	9	3	US-09-641-528B-23275	Sequence 23275, A
98	42.1	9	3	US-09-641-528B-33042	Sequence 33042, A
99	42.1	9	3	US-09-641-528B-37497	Sequence 37497, A

100 24 42.1 9 3 US-09-641-528B-48813 Sequence 48813, A

## ALIGNMENTS

RESULT 1  
US-08-019-073-19  
; Sequence 19, Application US/08019073  
; Patent No. 5559209  
; GENERAL INFORMATION:  
; APPLICANT: Nishimoto, Ikuo  
; TITLE OF INVENTION: REGULATOR REGIONS OF G  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3 5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/019,073  
; FILING DATE: 19930218  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/146001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-019-073-19

Query Match 100.0%; Score 57; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00047;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKDCGLF 10  
DB 1 KNNLKDCGLF 10  
|||||

RESULT 2  
US-08-429-964-50  
; Sequence 50, Application US/08429964  
; Patent No. 5962243  
; GENERAL INFORMATION:  
; APPLICANT: BROWN, MICHAEL S.  
; APPLICANT: GOLDSTEIN, JOSEPH L.  
; APPLICANT: REISS, YUVAL  
; APPLICANT: JAMES, GUY L.  
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL  
; TITLE OF INVENTION: TRANSFERASE INHIBITORS  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARNOLD, WHITE & DURKEE

; STREET: P.O. BOX 4433  
; CITY: HOUSTON  
; STATE: TEXAS  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/429,964  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/021,625  
; FILING DATE: 16-FEB-1993  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: US 07/822,011  
; FILING DATE: ABANDONED  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: PCT/US/91/02650  
; FILING DATE: 18-APR-1991  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: US 07/615,715  
; FILING DATE: 20-NOV-1990  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: US 07/510,706  
; FILING DATE: 18-APR-1990 (ABANDONED)  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PARKER, DAVID L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTSD:432/PAR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (713) 789-2679  
; TELEX: 79-0924  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-429-964-50

Query Match 100.0%; Score 57; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00047;  
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DB 1 KNNLKDCGLF 10  
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; GENERAL INFORMATION:  
; APPLICANT:  
; SEQUENCE CHARACTERISTICS:  
; SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.  
; SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.  
; SEQUENCE CHARACTERISTICS: REISS, YUVAL  
; SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.  
; ADDRESSEE: METHODS AND COMPOSITIONS FOR  
; ADDRESSEE: THE IDENTIFICATION,  
; ADDRESSEE: CHARACTERIZATION AND  
; ADDRESSEE: INHIBITION OF  
; ADDRESSEE: FARNESYLTRANSFERASE  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARNOLD, WHITE & DURKEE

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OM protein - protein search, using sw model

Run on: July 10, 2006, 17:00:16 ; Search time 42.5 Seconds  
(without alignments)  
108.992 Million cell updates/sec

Title: US-10-009-809-2

Perfect score: 57

Sequence: 1 KNNLKDCGLF 10

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Total number of hits satisfying chosen parameters: 284686

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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5	50	87.7	10	4	US-10-465-826-3
6	45	78.9	10	4	US-10-465-826-6
7	44	77.2	10	4	US-10-465-826-5
8	44	77.2	10	4	US-10-465-826-8
9	40	70.2	10	4	US-10-465-826-7
10	40	70.2	10	4	US-10-465-826-32
11	31	54.4	5	3	US-09-995-225-49
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13	31	54.4	5	4	US-10-333-844-11
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22	28	49.1	10	5	US-10-475-049A-9
23	28	49.1	10	5	US-10-475-049A-45
24	27	47.4	9	3	US-09-779-308-82
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29	27	47.4	9	3	US-09-779-308-485	Sequence 485, App
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34	27	47.4	10	3	US-09-779-308-227	Sequence 227, App
35	27	47.4	10	3	US-09-779-308-231	Sequence 231, App
36	27	47.4	10	3	US-09-779-308-420	Sequence 420, App
37	27	47.4	10	4	US-10-344-878-18	Sequence 18, Appl
38	27	47.4	10	5	US-10-922-806-12	Sequence 12, Appl
39	26	45.6	8	4	US-10-195-142-24	Sequence 24, Appl
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48	25	43.9	6	6	US-11-086-966-3	Sequence 3, Appl
49	25	43.9	8	3	US-09-908-322-90	Sequence 90, Appl
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51	25	43.9	9	3	US-09-775-803-10	Sequence 10, Appl
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53	25	43.9	10	3	US-09-572-404B-4019	Sequence 4019, Ap
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56	25	43.9	10	4	US-10-062-109A-309	Sequence 309, App
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66	24	42.1	8	4	US-10-473-495-29	Sequence 29, Appl
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69	24	42.1	9	4	US-10-100-303A-118	Sequence 118, App
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79	23	40.4	7	4	US-10-613-763-29	Sequence 29, Appl
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97	23	40.4	10	5	US-10-475-049A-48	Sequence 48, Appl
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## ALIGNMENTS

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RESULT 1
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; Sequence 31, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamar
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-465-826-31

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Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 4, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamar
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (10)..(10)
; OTHER INFORMATION: Para-amino Phenylalanine at position 10
US-10-465-826-4

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Db      1 KNNLKDCGLF 10
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RESULT 3
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; Sequence 2, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamar
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Decapeptide derived from Homo sapiens G-alpha-t
US-10-465-826-2

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Db      1 KNNLKDCGLF 10
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RESULT 4
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; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
; APPLICANT: Raz, Tamar
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES
; FILE REFERENCE: ALL/002 US
; CURRENT APPLICATION NUMBER: US/10/465,826
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: PCT/IL01/01186
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Decapeptide derived from Homo sapiens G-alpha-i3
US-10-465-826-1

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US-10-465-826-3
; Sequence 3, Application US/10465826
; Publication No. US20040137006A1
; GENERAL INFORMATION:
; APPLICANT: ALLERGENE LTD.
; APPLICANT: Eisenberg, Ronit
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OM protein - protein search, using sw model

Run on: July 10, 2006, 17:01:46 ; Search time 12.5 Seconds  
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21.466 Million cell updates/sec

Title: US-10-009-809-2

Perfect score: 57

Sequence: 1 KNNLKDCGLF 10

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Total number of hits satisfying chosen parameters: 10037

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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7	44	77.2	10	7	US-11-214-588-5
8	44	77.2	10	7	US-11-214-588-8
9	40	70.2	10	7	US-11-214-588-7
10	40	70.2	10	7	US-11-214-588-32
11	23	40.4	9	7	US-11-257-818-58
12	23	40.4	9	7	US-11-257-818-66
13	23	40.4	10	6	US-10-489-071-43
14	22	38.6	10	7	US-11-183-325-29
15	21	36.8	9	7	US-11-140-487A-1250
16	21	36.8	9	7	US-11-340-431-55
17	21	36.8	9	7	US-11-340-431-162
18	21	36.8	9	7	US-11-099-283B-179
19	21	36.8	10	7	US-11-122-986-709
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28	20	35.1	20	28	US-11-140-487A-1333
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34	20	35.1	20	34	US-11-140-487A-875
35	20	35.1	20	35	US-11-140-487A-819
36	20	35.1	20	36	US-11-122-986-622
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38	19	33.3	38	19	US-10-489-071-105
39	19	33.3	39	19	US-10-489-071-108
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42	19	33.3	42	19	US-10-506-334-20
43	19	33.3	43	19	US-11-332-378-65
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53	19	33.3	53	19	US-11-061-841-107
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95	17	29.8	95	17	US-11-140-487A-288
96	17	29.8	96	17	US-11-140-487A-280
97	17	29.8	97	17	US-11-140-487A-620
98	17	29.8	98	17	US-11-140-487A-1961



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Listing first 100 summaries

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4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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7	17	29.8	7	2	C56793
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9	16	28.1	8	2	PT0627
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13	15.5	27.2	10	2	S51912
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31	14	24.6	9	2	S27233	cardioactive pepti
32	14	24.6	9	2	S15850	vitamin D3 26-mono
33	14	24.6	10	2	E49033	T-cell receptor ga
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36	14	24.6	10	2	S70722	65.4K GTP-binding
37	14	24.6	10	2	F44644	neurotoxin-associa
38	14	24.6	10	2	S27873	hypothetical prote
39	13	22.8	6	2	I49424	cytotoxic T-lympho
40	13	22.8	7	2	A12016	formylglycinamide
41	13	22.8	8	2	S70727	IPgF protein - Shi
42	13	22.8	8	2	S78036	ribosomal protein
43	13	22.8	8	2	PT0522	T-cell receptor be
44	13	22.8	8	2	C61512	variant surface gl
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46	13	22.8	9	2	PC2021	oxytocin-related p
47	13	22.8	9	2	S06375	arginine vasotocin
48	13	22.8	9	2	B61364	vasotocin - common
49	13	22.8	10	2	A61131	hydrin 2 - bullfro
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51	13	22.8	10	2	C54226	light-harvesting p
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55	13	22.8	10	2	A33143	pneumadin - rat
56	12	21.1	4	2	S55238	pallidipin - assas
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59	12	21.1	5	2	A26830	mitosis inhibiting
60	12	21.1	6	2	PT0687	T-cell receptor be
61	12	21.1	6	2	PT0550	T-cell receptor be
62	12	21.1	7	2	S78024	ribosomal protein
63	12	21.1	7	2	PT0524	T-cell receptor be
64	12	21.1	7	2	PT0666	T-cell receptor be
65	12	21.1	7	2	PT0655	T-cell receptor be
66	12	21.1	7	2	PT0683	T-cell receptor be
67	12	21.1	8	2	PT0544	T-cell receptor be
68	12	21.1	8	2	PT0527	T-cell receptor be
69	12	21.1	8	2	PT0509	T-cell receptor be
70	12	21.1	8	2	PT0631	T-cell receptor be
71	12	21.1	8	2	PT0554	T-cell receptor be
72	12	21.1	8	2	S19288	acylase - Kluyvera
73	12	21.1	8	2	A21440	variant surface gl
74	12	21.1	8	2	E47393	neuropeptide calla
75	12	21.1	9	2	A61364	isotocin - common
76	12	21.1	9	2	I52974	seminal vesicle pr
77	12	21.1	9	2	PH0937	T-cell receptor be
78	12	21.1	9	2	JP0073	ribosomal protein
79	12	21.1	9	2	A61386	macrophage inhibit
80	12	21.1	9	2	I46016	cytokerin 4 - bo
81	12	21.1	10	2	S42282	paraspinal crystal
82	12	21.1	10	2	S62208	polyferredoxin - M
83	12	21.1	10	2	S23370	T-cell receptor al
84	12	21.1	10	2	B24736	inhibin beta-B cha
85	12	21.1	10	2	PH0807	T-cell receptor al
86	12	21.1	10	2	A39745	endo-glucosylceram
87	12	21.1	10	2	S30348	clotting protein -
88	12	21.1	10	2	S43631	cytochrome-c oxida
89	12	21.1	10	2	A60589	sperm-activating p
90	11	19.3	5	2	B45525	actin I - malaria
91	11	19.3	6	2	T11779	phosphoglycerate t
92	11	19.3	6	2	B45110	hypothetical prote
93	11	19.3	6	2	I65546	MHC H2-L antigen -
94	11	19.3	6	2	PT0630	T-cell receptor be
95	11	19.3	6	2	PT0619	T-cell receptor be
96	11	19.3	6	2	F41946	T-cell receptor ga
97	11	19.3	7	2	A34026	acetylcholinestera
98	11	19.3	7	2	S58797	serine/threonine-s
99	11	19.3	7	2	S45648	Na+-transporting A
100	11	19.3	7	2	S57274	triacylglycerol li

## ALIGNMENTS

```
RESULT 1
A11483
aspartate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)
N;Alternate names: aspartate aminotransferase, mitochondrial
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 20-Aug-1999
C;Accession: A11483
R;Campos-Cavieles, M.; Milatelin, C.P.
Biochem. J. 147, 275-281, 1975
A;Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mitoch
A;Reference number: A11483; MUID:76039441; PMID:1180894
A;Accession: A11483
A;Molecule type: protein
A;Residues: 1-7 <CM>
A;Cross-references: UNIPARC:UPI000017C59C
A;Experimental source: liver
C;Keywords: aminotransferase; mitochondrion; phosphoprotein; pyridoxal phosphate
F;2/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 36.8%; Score 21; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 KDCGLF 10
Db 2 KBWGLY 7

RESULT 2
S65726
hemoglobin, extracellular, chain b - earthworm (Lumbricus terrestris) (fragment)
C;Species: Lumbricus terrestris (Common earthworm)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65726
R;Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A;Title: Characterization of the constituent polypeptides of the extracellular hemoglobin
A;Reference number: S65721; MUID:96176855; PMID:8597573
A;Accession: S65726
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <FUS>
A;Cross-references: UNIPARC:UPI000017BD81

Query Match 35.1%; Score 20; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KDCG 8
Db 2 KQCG 5

RESULT 3
A47593
mercury resistance regulatory protein merR - Pseudomonas aeruginosa transposon Tn501 (fr
C;Species: Pseudomonas aeruginosa
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Aug-1998
C;Accession: A47593
R;O'Halloran, T.; Walsh, C.
Science 235, 211-214, 1987
A;Title: Metalloregulatory DNA-binding protein encoded by the merR gene: isolation and c
A;Reference number: A47593; MUID:87094195; PMID:3798107
A;Accession: A47593
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <ORH>
A;Cross-references: UNIPARC:UPI00001787DE
C;Superfamily: transcription repressor glrR
```

```
Query Match 33.3%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNNLKD 6
Db 2 ENNLN 7

RESULT 4
I67345
MHC H2-K-k cell surface glycoprotein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I67345
R;Archibald, A.L.; Thompson, N.A.; Kvist, S.
EMBO J. 5, 957-965, 1986
A;Title: A single nucleotide difference at the 3' end of an intron causes differential sp
A;Reference number: I53243; MUID:86247587; PMID:3013627
A;Accession: I67345
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: UNIPARC:UPI000011E8C5; GB:M26859; NID:gl199439; PIDN:AAA39612.1; PID:
C;Genetics: 6/1
A;introns: 6/1
C;Keywords: glycoprotein

Query Match 31.6%; Score 18; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LKDC 7
Db 1 LPDC 4

RESULT 5
A33882
cadmium-binding pentapeptide - downy thornapple
C;Species: Datura innoxia (downy thornapple)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C;Accession: A33882
R;Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A;Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant ce
A;Reference number: A94182; MUID:88016144; PMID:3477793
A;Accession: A33882
A;Molecule type: protein
A;Residues: 1-5 <JAC>
A;Cross-references: UNIPARC:UPI000017B088

Query Match 29.8%; Score 17; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 DCG 8
Db 3 ECG 5

RESULT 6
B33882
cadmium-binding heptapeptide - downy thornapple
C;Species: Datura innoxia (downy thornapple)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C;Accession: B33882
R;Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A;Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant ce
A;Reference number: A94182; MUID:88016144; PMID:3477793
A;Accession: B33882
A;Molecule type: protein
```



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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:57:41 ; Search time 80.5 Seconds  
(without alignments)  
114.909 Million cell updates/sec

Title: US-10-009-809-2  
Perfect score: 57  
Sequence: 1 KNNLKDCGLF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 3727

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	45.6	10	2	Q71VN2 mus musculus
2	23	40.4	9	2	Q5J2D2 ASPAW
3	22	38.6	9	2	Q6T3S6 CHLRE
4	20	35.1	8	2	Q7XB03 MAIZE
5	20	35.1	9	2	Q7X8P7 MAIZE
6	20	35.1	10	2	P82937 HORVU
7	19	33.3	7	2	Q9C5B3 ARATH
8	19	33.3	8	2	Q9AGP4 9MICC
9	19	33.3	10	2	Q718N9 9PARA
10	18	31.6	9	1	CWP07 LYCES
11	18	31.6	9	2	Q38340 9CAUD
12	18	31.6	10	1	CWP14 LYCES
13	18	31.6	10	2	Q48469 KLEPN
14	18	31.6	10	2	Q9R5N4 CLOBO
15	18	31.6	10	2	Q64G36 SCORO
16	17	29.8	7	2	O55184 RAT
17	17	29.8	10	1	SC43 TITCA
18	17	29.8	10	1	SYK CAMUP
19	17	29.8	10	2	Q8WTT4 HUMAN
20	16	28.1	8	2	Q6S842 DROSI
21	16	28.1	8	2	P92211 AGRCR
22	16	28.1	8	2	P92215 9POAL
23	16	28.1	8	2	P92219 9POAL
24	16	28.1	8	2	P92222 BROIN
25	16	28.1	8	2	P92227 CRIDE
26	16	28.1	8	2	P92373 9POAL
27	16	28.1	8	2	P92382 9POAL
28	16	28.1	8	2	P92384 9POAL
29	16	28.1	8	2	P92388 9POAL
30	16	28.1	8	2	P92391 HETFI
31	16	28.1	8	2	P92394 HORVU

32	16	28.1	8	2	P92404 LOPEL
33	16	28.1	8	2	P92422 PSAPR
34	16	28.1	8	2	P92426 PSEPI
35	16	28.1	8	2	P92428 9POAL
36	16	28.1	8	2	P92431 AEGTA
37	16	28.1	8	2	P92441 THIBE
38	16	28.1	8	2	P92443 TAECM
39	16	28.1	8	2	P93955 FESFE
40	16	28.1	8	2	P93957 FESSE
41	16	28.1	8	2	P93959 9POAL
42	16	28.1	8	2	P93961 PSARU
43	16	28.1	8	2	P93963 PSAST
44	16	28.1	8	2	P93965 SECT
45	16	28.1	8	2	P93966 AEGSP
46	16	28.1	8	2	P93970 9POAL
47	16	28.1	8	2	P93973 EREDI
48	16	28.1	8	2	P93981 9POAL
49	16	28.1	8	2	P93985 AEGCM
50	16	28.1	8	2	P93992 AUSVE
51	16	28.1	8	2	Q94VA0 9SAUR
52	16	28.1	9	1	FIBB PAPA
53	16	28.1	9	1	FIBB PAPA
54	16	28.1	9	1	FIBB THEGE
55	16	28.1	9	2	Q7R8X5 PLAYO
56	16	28.1	9	2	Q5EFY1 9BRYO
57	16	28.1	9	2	Q5EFY7 9BRYO
58	16	28.1	9	2	Q5EFZ0 9BRYO
59	16	28.1	9	2	Q8RKU3 BOREU
60	16	28.1	9	2	Q3TML8 MOUSE
61	16	28.1	9	2	Q99JF4 MOUSE
62	16	28.1	9	2	Q9QZAB MOUSE
63	16	28.1	10	1	PKV LOCHI
64	16	28.1	10	1	PKV PHVMO
65	16	28.1	10	1	XYNB DICB4
66	16	28.1	10	2	Q7RZ22 NEUCR
67	16	28.1	10	2	Q8NEY9 HUMAN
68	16	28.1	10	2	Q4G210 EULCO
69	16	28.1	10	2	Q4G211 LEMCA
70	16	28.1	10	2	Q4G212 TARSY
71	16	28.1	10	2	Q2KKK2 9BRYO
72	16	28.1	10	2	Q6JL97 NEIGO
73	16	28.1	10	2	Q71HU9 ICTSP
74	15	26.3	6	1	CWP27 ARATH
75	15	26.3	7	1	ASCL ALIAS
76	15	26.3	7	1	BRHP CONIM
77	15	26.3	7	2	Q8GL04 BOREU
78	15	26.3	7	2	Q8GL12 BOREU
79	15	26.3	8	2	Q35792 YEAST
80	15	26.3	8	2	Q71UR9 HUMAN
81	15	26.3	8	2	O02831 RABIT
82	15	26.3	8	2	Q79B39 BOREU
83	15	26.3	8	2	Q8G940 BOREU
84	15	26.3	8	2	Q8GL21 BOREU
85	15	26.3	8	2	Q80H91 9PARA
86	15	26.3	8	2	Q6UA69 CARCW
87	15	26.3	8	2	Q98TU5 XENLA
88	15	26.3	9	1	COW CONVE
89	15	26.3	9	1	NEUI BALPH
90	15	26.3	9	1	NEUI HIPAM
91	15	26.3	9	1	NEUI RABIT
92	15	26.3	9	1	NEUI TACAC
93	15	26.3	9	1	OXYT HYDCO
94	15	26.3	9	2	Q6UVK2 MALDO
95	15	26.3	9	2	Q31363 BOREU
96	15	26.3	9	2	Q6EKR5 YERPE
97	15	26.3	9	2	Q712A6 SINSE
98	15	26.3	9	2	Q8GL26 BOREU
99	15	26.3	9	2	Q9R3T0 BORAF
100	15	26.3	9	2	Q9R792 BOREU

ALIGNMENTS

```
RESULT 1
Q71VN2_MOUSE PRELIMINARY; PRT; 10 AA.
ID Q71VN2_MOUSE PRELIMINARY; PRT; 10 AA.
AC Q71VN2_MOUSE PRELIMINARY; PRT; 10 AA.
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Secretory leukoprotease inhibitor (Fragment).
GN Name=Slpi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129SV;
RX MEDLINE=99061820; PubMed=9843921;
RA Kikuchi T., Abe T., Hoshi S., Matsubara N., Tominaga Y., Satoh K.,
RA Nukiwa T.;
RT "Structure of the murine secretory leukoprotease inhibitor (Slpi) gene
RT and chromosomal localization of the human and murine SLPI genes.";
RL Am. J. Respir. Cell Mol. Biol. 19:875-880(1998).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF002720; AAD09308.1; -; Genomic_DNA.
DR MGI; MGI:109297; Slpi.
DR GO; GO:0005615; C:extracellular space; RCA.
KW Protease.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1096 MW; 8651EB6727287EA5 CRC64;

Query Match 45.6%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LKDCGL 9
DB : |||
1 MKSCGL 6

RESULT 2
Q5J2D2_ASPAW PRELIMINARY; PRT; 9 AA.
ID Q5J2D2_ASPAW PRELIMINARY; PRT; 9 AA.
AC Q5J2D2_ASPAW PRELIMINARY; PRT; 9 AA.
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Glucosamine-6-phosphate synthase (Fragment).
GN Name=gfaA;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CBS115.52;
RX PubMed=15589992; DOI=10.1016/j.fgb.2004.06.009;
RA Michieles C.B., Arentshorst M., Ram A.F., van den Hondel C.A.;
RT "Agrobacterium-mediated transformation leads to improved gene
RT replacement efficiency in Aspergillus awamori.";
RL Fungal Genet. Biol. 42:9-19(2005).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY530808; AAT01419.1; -; Genomic_DNA.
DR InterPro; IPR000583; GATase.2.
DR PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
FT NON_TER 9
```

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SQ SEQUENCE 9 AA; 1017 MW; 94794B5879C0587E CRC64;

Query Match 40.4%; Score 23; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CGLF 10
DB : |||
2 CGIF 5

RESULT 3
Q6T3S6_CHLRE PRELIMINARY; PRT; 9 AA.
ID Q6T3S6_CHLRE PRELIMINARY; PRT; 9 AA.
AC Q6T3S6_CHLRE PRELIMINARY; PRT; 9 AA.
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Cyclophilin 1 (Fragment).
GN Name=Cyp1;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
OC Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CC-2290;
RX MEDLINE=22570934; PubMed=12684385; DOI=10.1128/EC.2.2.362-379.2003;
RA Kathir P., LaVoie M., Brazelton W.J., Haas N.A., Lefebvre P.A.,
RA Silflow C.D.;
RT "Molecular map of the Chlamydomonas reinhardtii nuclear genome.";
RL Eukaryot. Cell 2:362-379(2003).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY437923; AAR22883.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 9 AA; 861 MW; 10D236D87EBADD0 CRC64;

Query Match 38.6%; Score 22; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LKDCG 8
DB : |||
2 IADCG 6

RESULT 4
Q7XB03_MAIZE PRELIMINARY; PRT; 8 AA.
ID Q7XB03_MAIZE PRELIMINARY; PRT; 8 AA.
AC Q7XB03_MAIZE PRELIMINARY; PRT; 8 AA.
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Phytoene synthase 2 (Fragment).
GN Name=psy2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Y-3;
RX MEDLINE=2279048; PubMed=12897253; DOI=10.1105/tpc.012526;
RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT "Contrasting effects of selection on sequence diversity and linkage
RT disequilibrium at two phytoene synthase loci.";
RL Plant Cell 15:1795-1806(2003).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
```

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 14, 2006, 06:44:08 ; Search time 81 Seconds  
(without alignments)  
90.314 Million cell updates/sec

Title: US-10-009-809-3

Perfect score: 70

Sequence: 1 AAVALLPAVLALLAP 16

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 859960

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A\_Geneseq\_8.\*

1: Geneseq1980s.\*

2: Geneseq1990s.\*

3: Geneseq2000s.\*

4: Geneseq2001s.\*

5: Geneseq2002s.\*

6: Geneseq2003as.\*

7: Geneseq2003bs.\*

8: Geneseq2004s.\*

9: Geneseq2005s.\*

10: Geneseq2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	16	2	AAR87629 Signal pe
2	70	100.0	16	2	AAR37753 Chimeric
3	70	100.0	16	2	AAW56394 MEM polyp
4	70	100.0	16	2	AAW48689 Signal pe
5	70	100.0	16	2	AAW53769 PKR pepti
6	70	100.0	16	2	AAW13506 Signal se
7	70	100.0	16	3	AAV67954 Kaposi's
8	70	100.0	16	3	AAV55815 Fibroblas
9	70	100.0	16	4	AAE02979 Hydrophob
10	70	100.0	16	4	AAU97005 CCAAT enh
11	70	100.0	16	4	AAE1949 Membrane
12	70	100.0	16	4	AAU03154 Peptide K
13	70	100.0	16	4	AAV72476 Kaposi fi
14	70	100.0	16	5	ABG78989 Cell pene
15	70	100.0	16	5	AAU10399 Membrane
16	70	100.0	16	5	AAE15613 Kaposi's
17	70	100.0	16	5	AAU78349 Signal se
18	70	100.0	16	5	AAE26128 Kaposi fi
19	70	100.0	16	5	ABG75507 Signal-se
20	70	100.0	16	5	ABB81177 Signal se
21	70	100.0	16	5	AAE23686 Fluoresce
22	70	100.0	16	6	ABR82543 Signal se
23	70	100.0	16	6	ABR84444 K-FGF sig

24	70	100.0	16	6	AAE33897	Kaposi's
25	70	100.0	16	6	ABU09984	Kaposi's
26	70	100.0	16	6	ADC22454	Protein-d
27	70	100.0	16	7	ADF78064	Human mem
28	70	100.0	16	7	ADG28017	Kaposi FG
29	70	100.0	16	7	ADH76184	Transduct
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34	70	100.0	16	8	ADJ78875	N-termina
35	70	100.0	16	8	ADL14686	Cardiant
36	70	100.0	16	8	ADK15574	Membrane
37	70	100.0	16	8	ADO26466	Kaposi's
38	70	100.0	16	8	ADM97016	Botulinum
39	70	100.0	16	8	ADO25265	Signal se
40	70	100.0	16	8	ADP08148	Small int
41	70	100.0	16	8	ADP08145	Small int
42	70	100.0	16	8	ADQ60179	Human her
43	70	100.0	16	8	ADR31972	Heat choc
44	70	100.0	16	8	ADR82252	Membrane
45	70	100.0	16	8	ADU15734	MUC1-PDZ
46	70	100.0	16	8	ADT61097	Novel int
47	70	100.0	16	8	ADU07192	Membrane
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51	70	100.0	16	8	ADU26590	Cell perm
52	70	100.0	16	8	ABE19669	Novel gen
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60	70	100.0	16	9	ADZ69395	HSP20 tra
61	70	100.0	16	9	AEA98089	Signal se
62	70	100.0	16	9	AEA33043	Kaposi fi
63	70	100.0	16	9	AEA36361	Basic dom
64	70	100.0	16	9	ABE17248	Human mem
65	70	100.0	16	9	AEA43032	Membrane
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67	70	100.0	16	9	AEC78139	NRIF3 der
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72	70	100.0	16	10	ABE84512	Signal se
73	70	100.0	16	10	ABE91963	Kaposi FG
74	70	100.0	16	10	ABE48449	Signal se
75	70	100.0	16	10	AEF42977	Kaposi fi
76	70	100.0	16	10	AEF90254	Signal se
77	70	100.0	16	10	AEF99409	Hydrophob
78	63	90.0	15	2	AAW56398	Preferred
79	63	90.0	15	3	AAV55819	Signal se
80	63	90.0	15	5	AAU78913	Fibroblas
81	63	90.0	15	9	ADZ68060	Kaposi's
82	63	90.0	16	3	AAV67268	Fibroblas
83	58	82.9	15	6	AAO16667	Human cel
84	55.5	79.3	15	4	AAU03166	Kaposi fi
85	46	65.7	14	4	AAE12500	Membrane
86	46	65.7	14	9	ABE09938	Antiviral
87	39	55.7	11	4	AAE12491	Membrane
88	39	55.7	11	9	ABE09930	Antiviral
89	39	55.7	13	4	AAE12480	Membrane
90	39	55.7	13	4	AAE12497	Membrane
91	39	55.7	13	9	ABE09919	Antiviral
92	39	55.7	16	4	AAE12498	Membrane
93	39	55.7	16	9	ABE09936	Antiviral
94	37	52.9	14	4	AAE12504	Membrane
95	37	52.9	14	9	ABE09942	Antiviral
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97 34 48.6 10 6 AAE32592 Aae32592 West Nile  
 98 34 48.6 10 6 AAE32518 Aae32518 West Nile  
 99 33.5 47.9 13 5 ABG98327 ABG98327 Secreted  
 100 33 47.1 15 9 ADX24978 ADX24978 Human pro

## ALIGNMENTS

RESULT 1  
 AAR87629 AAR87629 standard; peptide; 16 AA.  
 XX  
 AC AAR87629;  
 XX  
 DT 23-JUL-1996 (first entry)  
 XX  
 DE Signal peptide of K-FGF.  
 XX  
 KW Signal peptide; K-FGF; Kaposi fibroblast growth factor; FGF; inhibition;  
 KW growth factor; nuclear localisation sequence; growth regulation; p50;  
 KW tumour cell; transcription factor; NF-kappaB; therapy.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9534295-A1.  
 XX  
 PD 21-DEC-1995.  
 XX  
 PF 13-JUN-1995; 95WO-US007539.  
 XX  
 PR 13-JUN-1994; 94US-00258852.  
 XX  
 PA (UYVA-) UNIV VANDERBILT.  
 XX  
 PI Lin Y, Hawiger JJ;  
 XX  
 DR WPI; 1996-049396/05.  
 XX  
 PT Importing biologically active molecules ex vivo or in vivo into cells -  
 PT useful in regulation of cell growth and inhibition of gene expression.  
 XX  
 PS Claim 5; Page 35; 47pp; English.  
 XX  
 CC This sequence represents the signal peptide of Kaposi fibroblast growth  
 CC factor (K-FGF). This sequence is an importation competent signal peptide  
 CC (SP), and is used in the methods of the invention. These methods are  
 CC designed to import a biologically active molecule (BAM) into a cell  
 CC (either ex vivo or in vivo). The methods comprise administering to the  
 CC cell a complex comprising the BAM linked to an importation competent SP  
 CC (such as this sequence), and thereby importing the BAM into the cell. The  
 CC BAM-SP complex is optionally linked to a nuclear localisation sequence  
 CC peptide (NLS), to achieve importation into the nucleus of a cell. This  
 CC method can be used to regulate the growth of a cell, e.g. tumour cells.  
 CC Also, for inhibiting the expression of a gene. Genes regulated by a  
 CC transcription factor such as NF-kappaB are inhibited by a complex  
 CC comprising an SP linked to an NLS of the active p50 subunit of NF-kappaB.  
 CC This method imports BAM's into a cell using mechanisms naturally occurring  
 CC in cells, thereby avoiding damaging the target cells. It can also be used  
 CC to import molecules into large numbers of cells, including organs  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 70; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.0008;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AAVALLPVALLALLAP 16  
 DB 1 AAVALLPVALLALLAP 16

RESULT 2

AAW37753  
 ID AAW37753 standard; peptide; 16 AA.  
 XX  
 AC AAW37753;  
 XX  
 DT 20-JUL-1998 (first entry)  
 XX  
 DE Chimeric peptide 1.  
 XX  
 KW Chimeric peptide; signal peptide; ras gene product; mutation;  
 KW leukaemic cell; bone marrow cell; transduction.  
 XX  
 OS Synthetic.  
 XX  
 PN US5736394-A.  
 XX  
 PD 07-APR-1998.  
 XX  
 PF 03-MAY-1996; 96US-00642493.  
 XX  
 PR 03-MAY-1996; 96US-00642493.  
 XX  
 PA (BOST-) BOSTON BIOMEDICAL RES INST.  
 XX  
 PI Coleman PS, Sheldon K;  
 XX  
 DR WPI; 1998-239216/21.  
 XX  
 PT Cellular uptake of specific modified peptide(s) - useful for covalent  
 PT bonding to, and inactivation of intracellular proteins.  
 XX  
 PS Disclosure; Col 3; 11pp; English.  
 XX  
 CC This amino acid sequence is of a chimeric peptide comprising a known  
 CC signal peptide, and is used in the method of invention as a way of  
 CC introducing a peptide into a cell. They are also useful for specifically  
 CC covalently binding a peptide to a target protein in a cell and  
 CC irreversibly block a binding site on the protein e.g. the peptide can be  
 CC used to inactivate the ras gene product which is mutated in leukaemic  
 CC cells and essential for survival, but not essential in normal bone marrow  
 CC cells. It can also be used to deduce the role of different proteins in  
 CC signal transduction pathways by systematically inactivating them and  
 CC seeing the resultant effects  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 70; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.0008;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AAVALLPVALLALLAP 16  
 DB 1 AAVALLPVALLALLAP 16  
 RESULT 3  
 AAW56394  
 ID AAW56394 standard; peptide; 16 AA.  
 XX  
 AC AAW56394;  
 XX  
 DT 05-AUG-1998 (first entry)  
 XX  
 DE MEM polypeptide used to inhibit kappa-Ig light chain expression.  
 XX  
 KW SV40MEM polypeptide; signal peptide; fibroblast growth factor;  
 KW SV40 large antigen; nuclear localisation signal; NLS;  
 KW immunosuppressive activity; inhibition; nuclear translocation inhibitor;  
 KW kappa immunoglobulin light chain expression; S. typhosa LPS;  
 KW nuclear translocation; treatment; immune disorder; autoimmune disease;  
 KW hypersensitivity; sepsis; prevention; septic shock; antiviral agent;  
 KW tumour growth suppressor; MEM.  
 XX

GenCore version 5.1.9  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM protein - protein search, using sw model  
 Run on: July 10, 2006, 17:03:01 ; Search time 24 Seconds  
 (without alignments)  
 58.354 Million cell updates/sec

Title: US-10-009-809-3

Perfect score: 70

Sequence: 1 AAVALLPAVLLALLAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 257069

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued patents\_AA:  
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 4: /EMC Cellerai\_SIDS3/ptodata/2/iaa/H COMB.pap.\*  
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 7: /EMC Cellerai\_SIDS3/ptodata/2/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	70	100.0	16	1	US-08-258-852-5
3	70	100.0	16	1	US-08-928-958-4
4	70	100.0	16	1	US-09-072-429-4
5	70	100.0	16	2	US-08-964-302A-3
6	70	100.0	16	2	US-09-170-754B-5
7	70	100.0	16	2	US-09-441-416A-3
8	70	100.0	16	2	US-09-411-706-1
9	70	100.0	16	2	US-09-230-548-19
10	70	100.0	16	2	US-09-450-071A-5
11	70	100.0	16	2	US-09-935-032-1
12	70	100.0	16	2	US-10-083-889-7
13	70	100.0	16	2	US-10-116-288A-23
14	70	100.0	16	2	US-10-144-549-18
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16	70	100.0	16	5	PCT-US95-07539-5
17	63	90.0	15	1	US-08-928-958-8
18	63	90.0	15	1	US-09-072-429-8
19	63	90.0	16	2	US-09-720-039-1
20	33	47.1	14	3	US-10-000-986A-156
21	32	45.7	14	3	US-10-000-986A-146
22	31	44.3	15	2	US-09-671-089-2
23	31	44.3	16	2	US-09-671-089-3
24	31	44.3	16	2	US-09-671-089-48
25	30	42.9	14	1	US-07-908-317-17
26	30	42.9	14	3	US-10-000-986A-157

27	30	42.9	14	3	US-10-000-986A-158
28	30	42.9	14	5	PCT-US93-06171-17
29	30	42.9	16	2	US-10-068-426-13
30	28	40.0	8	2	US-08-444-818-475
31	28	40.0	15	2	US-09-009-953-176
32	28	40.0	15	2	US-09-009-953-183
33	27	38.6	9	2	US-09-845-583A-17
34	27	38.6	11	2	US-09-186-170-5
35	27	38.6	11	2	US-09-562-868-5
36	27	38.6	11	2	US-10-116-288A-5
37	27	38.6	11	2	US-09-671-089-15
38	27	38.6	12	2	US-09-186-170-1
39	27	38.6	12	2	US-09-562-868-1
40	27	38.6	12	2	US-09-997-465B-4
41	27	38.6	12	2	US-10-083-889-8
42	27	38.6	12	2	US-10-116-288A-1
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45	27	38.6	12	2	US-10-144-549-19
46	27	38.6	13	2	US-09-237-357-482
47	27	38.6	13	2	US-09-671-089-6
48	27	38.6	13	2	US-09-973-278-538
49	27	38.6	16	1	US-08-169-948B-36
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51	27	38.6	16	2	US-08-382-452D-36
52	27	38.6	16	2	US-08-507-362A-20
53	27	38.6	16	2	US-09-916-494A-36
54	27	38.6	16	2	US-09-671-089-5
55	27	38.6	16	3	US-10-379-978-20
56	26	37.1	13	5	PCT-US94-10257A-57
57	26	37.1	14	1	US-08-503-226B-41
58	26	37.1	14	1	US-08-503-326B-42
59	26	37.1	14	2	US-08-721-458B-41
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61	26	37.1	15	3	US-09-641-528B-46855
62	26	37.1	15	3	US-09-641-528B-46871
63	26	37.1	16	2	US-09-434-345-5
64	26	37.1	16	7	5486473-16
65	25	35.7	9	2	US-09-492-543-55
66	25	35.7	9	2	US-09-492-543-105
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68	25	35.7	9	2	US-10-172-597-55
69	25	35.7	9	2	US-10-172-597-105
70	25	35.7	9	2	US-10-172-597-112
71	25	35.7	10	2	US-09-319-730-9
72	25	35.7	10	2	US-09-936-885A-25
73	25	35.7	14	1	US-07-908-317-34
74	25	35.7	14	1	US-07-961-837-7
75	25	35.7	14	5	PCT-US93-06171-34
76	25	35.7	16	1	US-08-156-552A-6
77	25	35.7	16	2	US-09-035-249A-6
78	24.5	35.0	10	2	US-09-186-170-4
79	24.5	35.0	10	2	US-09-562-868-4
80	24.5	35.0	10	2	US-10-116-288A-4
81	24.5	35.0	12	2	US-09-671-089-16
82	24.5	35.0	12	2	US-09-671-089-59
83	24.5	35.0	14	2	US-09-671-089-7
84	24.5	35.0	14	2	US-09-671-089-58
85	24	34.3	8	2	US-09-865-548A-46
86	24	34.3	9	2	US-09-186-170-3
87	24	34.3	9	2	US-09-185-501B-7
88	24	34.3	9	2	US-09-562-868-3
89	24	34.3	9	2	US-10-116-288A-3
90	24	34.3	9	2	US-09-671-089-17
91	24	34.3	9	2	US-09-865-548A-89
92	24	34.3	9	3	US-09-641-528B-16979
93	24	34.3	9	3	US-09-641-528B-25892
94	24	34.3	9	3	US-09-641-528B-48945
95	24	34.3	10	1	US-08-371-930-11
96	24	34.3	10	3	US-09-641-528B-3843
97	24	34.3	10	3	US-09-641-528B-12934
98	24	34.3	10	3	US-09-641-528B-25837
99	24	34.3	10	5	PCT-US94-01712-11

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 Sequence 16979, A  
 Sequence 25892, A  
 Sequence 48945, A  
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 Sequence 12934, A  
 Sequence 25837, A  
 Sequence 11, Appl

100 24 34.3 11 2 US-09-472-087-103 Sequence 103, App

## ALIGNMENTS

RESULT 1  
US-08-642-493-1  
; Sequence 1, Application US/08642493  
; Patent No. 5736394  
; GENERAL INFORMATION:  
; APPLICANT: Coleman, Peter S.  
; APPLICANT: Sheldon, Katherine  
; TITLE OF INVENTION: CELLULAR UPTAKE OF MODIFIED PEPTIDES  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: ME  
; COUNTRY: USA  
; ZIP: 03911

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/642,493  
; FILING DATE:  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M.  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: BBRI-9602  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-642-493-1

Query Match 100.0%; Score 70; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00023;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAVALPVLALLAP 16  
| | | | | | | | | | | | | | | |  
Db 1 AAVALPVLALLAP 16  
| | | | | | | | | | | | | | | |  
RESULT 2  
US-08-258-852-5  
; Sequence 5, Application US/08258852  
; Patent No. 5807746  
; GENERAL INFORMATION:  
; APPLICANT: Lin, Yao-Zhong  
; APPLICANT: Hawiger, Jack J.  
; TITLE OF INVENTION: A NOVEL METHOD FOR IMPORTING  
; BIOLOGICALLY ACTIVE MOLECULES INTO CELLS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
; STREET: 127 Peachtree Street, N.E.  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303-1811

Query Match 100.0%; Score 70; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00023;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAVALPVLALLAP 16  
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Db 1 AAVALPVLALLAP 16  
| | | | | | | | | | | | | | | |

RESULT 3  
US-08-928-958-4  
; Sequence 4, Application US/08928958  
; Patent No. 5877282  
; GENERAL INFORMATION:  
; APPLICANT: NADLER, STEVEN G.  
; APPLICANT: CLEVELAND, JEFFREY S.  
; APPLICANT: BLAKE, JAMES  
; APPLICANT: HAFFAR, OMAR K.  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN  
; TRANSLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND  
; METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROBINS & ASSOCIATES  
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
; CITY: MENLO PARK  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/928,958  
; FILING DATE: 12-SEP-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/026978  
; FILING DATE: 20-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ROBINS, ROBERTA L.

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/258,852  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pertyman, David G.  
; REGISTRATION NUMBER: 33,438  
; REFERENCE/DOCKET NUMBER: 2200.021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404/688-0770  
; TELEFAX: 404/688-9880  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..16  
; OTHER INFORMATION: /label= a  
; OTHER INFORMATION: /note= "Signal peptide of K-FGF"

US-08-258-852-5  
Query Match 100.0%; Score 70; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00023;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAVALPVLALLAP 16  
| | | | | | | | | | | | | | | |  
Db 1 AAVALPVLALLAP 16  
| | | | | | | | | | | | | | | |

RESULT 3  
US-08-928-958-4  
; Sequence 4, Application US/08928958  
; Patent No. 5877282  
; GENERAL INFORMATION:  
; APPLICANT: NADLER, STEVEN G.  
; APPLICANT: CLEVELAND, JEFFREY S.  
; APPLICANT: BLAKE, JAMES  
; APPLICANT: HAFFAR, OMAR K.  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN  
; TRANSLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND  
; METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROBINS & ASSOCIATES  
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
; CITY: MENLO PARK  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/928,958  
; FILING DATE: 12-SEP-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/026978  
; FILING DATE: 20-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ROBINS, ROBERTA L.

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: July 10, 2006, 17:04:01 ; Search time 49 Seconds  
(without alignments)  
151.254 Million cell updates/sec

Title: US-10-009-809-3

Perfect score: 70

Sequence: 1 AAVALLPAVLLALLAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 408280

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	70	100.0	16	3	US-09-962-967A-3
5	70	100.0	16	3	US-09-965-876A-3
6	70	100.0	16	3	US-09-789-831-12
7	70	100.0	16	4	US-10-226-956-285
8	70	100.0	16	4	US-10-077-555-7
9	70	100.0	16	4	US-10-211-088-303
10	70	100.0	16	4	US-10-136-738-18
11	70	100.0	16	4	US-10-156-570A-26
12	70	100.0	16	4	US-10-144-549-18
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15	70	100.0	16	4	US-10-261-161-22
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18	70	100.0	16	4	US-10-688-299-18
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26	70	100.0	16	5	US-10-700-971C-7
27	70	100.0	16	5	US-10-927-262A-45
28	70	100.0	16	5	US-10-878-175B-37
29	70	100.0	16	5	US-10-991-286A-46
30	70	100.0	16	5	US-10-899-912A-39
31	70	100.0	16	5	US-10-985-426-16
32	70	100.0	16	5	US-10-909-769-1
33	70	100.0	16	5	US-10-535-780-2
34	70	100.0	16	5	US-10-923-112A-37
35	70	100.0	16	6	US-11-027-967-4
36	70	100.0	16	6	US-11-004-795A-117
37	70	100.0	16	6	US-11-004-379-22
38	70	100.0	16	6	US-11-004-794A-101
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40	70	100.0	16	6	US-11-016-542-6
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47	46	65.7	14	3	US-09-777-560-24
48	46	65.7	14	6	US-11-001-674-23
49	39	55.7	13	3	US-09-777-560-4
50	39	55.7	13	3	US-09-777-560-21
51	39	55.7	13	6	US-11-001-674-4
52	39	55.7	16	3	US-09-777-560-22
53	39	55.7	16	6	US-11-001-674-21
54	37	52.9	14	3	US-09-777-560-28
55	37	52.9	14	6	US-11-001-674-27
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59	33	47.1	15	5	US-10-857-484-6133
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62	33	47.1	16	6	US-11-223-699A-5
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86	31	44.3	15	4	US-10-764-235-2
87	31	44.3	15	5	US-10-850-873-2
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Sequence 40, Appl  
Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-09-214-371-45  
; Sequence 45, Application US/09214371B  
; Patent No. US20010018511A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Pickseley, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
; FILE REFERENCE: 4-20937/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/214,371B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-07-04  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 45  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
US-09-214-371-45

Query Match 100.0%; Score 70; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVALPAVLLALLAP 16  
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Db 1 AAVALPAVLLALLAP 16

RESULT 2  
US-09-811-870-5  
; Sequence 5, Application US/09811870  
; Publication No. US20020031820A1  
; GENERAL INFORMATION:  
; APPLICANT: Cole, Philip  
; APPLICANT: Parang, Keykavous  
; APPLICANT: Abloogu, Ararat  
; APPLICANT: Kohanski, Ronald  
; APPLICANT: Courtney, Aliya  
; TITLE OF INVENTION: Bisubstrate Inhibitors of Kinases  
; FILE REFERENCE: 001107.00108  
; CURRENT APPLICATION NUMBER: US/09/811,870  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/190,799  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: kinase substrates  
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Query Match 100.0%; Score 70; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAVALPAVLLALLAP 16

RESULT 3  
US-09-785-802A-9  
; Sequence 9, Application US/09785802A  
; Patent No. US20020151004A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig, Roger  
; TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME  
; FILE REFERENCE: 11067/2035  
; CURRENT APPLICATION NUMBER: US/09/785,802A  
; CURRENT FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: US 09/748,06  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/748,789  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 9  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-785-802A-9

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Best Local Similarity 100.0%; Pred. No. 0.0013;  
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RESULT 4  
US-09-962-967A-3  
; Sequence 3, Application US/09962967A  
; Publication No. US20030004112A1  
; GENERAL INFORMATION:  
; APPLICANT: Potter, David A.  
; APPLICANT: Skolnik, Paul R.  
; TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF CALPAIN  
; FILE REFERENCE: 00398-140002  
; CURRENT APPLICATION NUMBER: US/09/962,967A  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 09/441,416  
; PRIOR FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: US 08/964,302  
; PRIOR FILING DATE: 1997-11-04  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetically generated peptide  
US-09-962-967A-3

Query Match 100.0%; Score 70; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAVALPAVLLALLAP 16

RESULT 5  
US-09-965-876A-3  
; Sequence 3, Application US/09965876A



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OM protein - protein search, using sw model

Run on: July 10, 2006, 17:04:31 ; Search time 9 Seconds  
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Title: US-10-009-809-3

Perfect score:

Sequence: 1 AAVALLPAVLLALLAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 20584

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:\*

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4: /ENC Celleria SIDS3 /ptodata/2/pubpaas/US08 NEW PUB DEP:  
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8: /ENC Celleria SIDS3 /ptodata/2/pubpaas/US60 NEW PUB DEP:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES								
Result No.	Score		Query Match		Length	DB	ID	Description
1	70	100.0	16	7	US-11-214-588-27			Sequence 27, Appl
2	70	100.0	16	7	US-11-263-230-296			Sequence 296, App
3	70	100.0	16	7	US-11-259-133-109			Sequence 109, App
4	70	100.0	16	7	US-11-259-266-37			Sequence 37, Appl
5	70	100.0	16	7	US-11-259-267-37			Sequence 37, Appl
6	63	90.0	15	7	US-11-251-734-3			Sequence 3, Appli
7	39	58.7	10	7	US-11-223-610-61			Sequence 61, Appl
8	31	44.3	15	7	US-11-303-372-2			Sequence 2, Appli
9	31	44.3	15	7	US-11-303-372-3			Sequence 3, Appli
10	31	44.3	15	7	US-11-303-372-60			Sequence 60, Appl
11	31	44.3	15	7	US-11-303-372-61			Sequence 61, Appl
12	31	44.3	16	7	US-11-303-372-48			Sequence 48, Appl
13	30	42.9	16	7	US-11-257-581-13			Sequence 13, Appl
14	30	42.9	16	7	US-11-257-581-13			Sequence 13, Appl
15	28	40.0	9	7	US-11-140-487A-1481			Sequence 1481, Ap
16	28	40.0	10	7	US-11-140-487A-969			Sequence 969, App
17	28	40.0	14	7	US-11-140-487A-2121			Sequence 2121, Ap
18	28	40.0	14	7	US-11-140-487A-2126			Sequence 2126, Ap
19	28	40.0	15	7	US-11-140-487A-2179			Sequence 2179, Ap
20	28	40.0	15	7	US-11-140-487A-2236			Sequence 2236, Ap
21	27	38.6	9	7	US-11-140-487A-1389			Sequence 1389, Ap
22	27	38.6	9	7	US-11-340-431-34			Sequence 34, Appl
23	27	38.6	9	7	US-11-340-431-35			Sequence 35, Appl
24	27	38.6	9	7	US-11-340-431-58			Sequence 58, Appl
25	27	38.6	9	7	US-11-340-431-255			Sequence 255, App

99 21 30.0 15 7 US-11-140-487A-2131 Sequence 2131, Ap  
100 21 30.0 15 7 US-11-140-487A-2139 Sequence 2139, Ap

## ALIGNMENTS

RESULT 1  
US-11-214-588-27  
; Sequence 27, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; APPLICANT: Raz, Tamar  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 27  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-214-588-27

Query Match 100.0%; Score 70; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVALLPAVLALLAP 16  
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DB 1 AAVALLPAVLALLAP 16

RESULT 2  
US-11-263-230-296  
; Sequence 296, Application US/11263230  
; Publication No. US20060115485A1  
; GENERAL INFORMATION:  
; APPLICANT: Losonsky, Genevieve  
; APPLICANT: Connor, Edward M.  
; APPLICANT: Young, James F.  
; APPLICANT: Wu, Herren  
; APPLICANT: Dall'Acqua, William  
; TITLE OF INVENTION: Methods of Preventing and Treating RSV Infections  
; FILE REFERENCE: 10271-174-999  
; CURRENT APPLICATION NUMBER: US/11/263,230  
; CURRENT FILING DATE: 2005-10-31  
; PRIOR APPLICATION NUMBER: 60/623,821  
; PRIOR FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: 60/675,724  
; PRIOR FILING DATE: 2005-04-27  
; PRIOR APPLICATION NUMBER: 60/681,233  
; PRIOR FILING DATE: 2005-05-13  
; PRIOR APPLICATION NUMBER: 60/718,719  
; PRIOR FILING DATE: 2005-09-21  
; PRIOR APPLICATION NUMBER: 60/727,042  
; PRIOR FILING DATE: 2005-10-14  
; PRIOR APPLICATION NUMBER: 60/727,043  
; PRIOR FILING DATE: 2005-10-14  
; NUMBER OF SEQ ID NOS: 1496  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 296  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

; OTHER INFORMATION: intrabody  
US-11-263-230-296

Query Match 100.0%; Score 70; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVALLPAVLALLAP 16  
|||||  
DB 1 AAVALLPAVLALLAP 16

RESULT 3  
US-11-259-133-109  
; Sequence 109, Application US/11259133  
; Publication No. US20060121042A1  
; GENERAL INFORMATION:  
; APPLICANT: Dall'Acqua, William  
; APPLICANT: Damschroder, Melissa  
; APPLICANT: Kinch, Michael  
; APPLICANT: Carles-Kinch, Kelly  
; TITLE OF INVENTION: MODULATION OF ANTIBODY SPECIFICITY BY TAILORING THE AFFINITY TO  
; TITLE OF INVENTION: COGNATE ANTIGENS  
; FILE REFERENCE: EP7000US  
; CURRENT APPLICATION NUMBER: US/11/259,133  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: 60/622,711  
; PRIOR FILING DATE: 2004-10-27  
; PRIOR APPLICATION NUMBER: 60/717,209  
; PRIOR FILING DATE: 2005-09-16  
; NUMBER OF SEQ ID NOS: 205  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 109  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-259-133-109

Query Match 100.0%; Score 70; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVALLPAVLALLAP 16  
|||||  
DB 1 AAVALLPAVLALLAP 16

RESULT 4  
US-11-259-266-37  
; Sequence 37, Application US/11259266  
; Publication No. US20060121043A1  
; GENERAL INFORMATION:  
; APPLICANT: Kinch, Michael  
; APPLICANT: Carles-Kinch, Kelly  
; TITLE OF INVENTION: Use of Modulators of EphA2 and EphrinA1 for the Treatment and Pre-  
; TITLE OF INVENTION: of Infections  
; FILE REFERENCE: EP3500US  
; CURRENT APPLICATION NUMBER: US/11/259,266  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: 60/622,489  
; PRIOR FILING DATE: 2004-10-27  
; PRIOR APPLICATION NUMBER: 60/705,705  
; PRIOR FILING DATE: 2005-08-03  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 37  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-259-266-37

Query Match 100.0%; Score 70; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 17:02:29 ; Search time 22 seconds  
(without alignments)  
69.976 Million cell updates/sec

Title: US-10-009-809-3

Perfect score: 70

Sequence: 1 AAVALLPAVILLALLAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2773

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR\_80:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	34.3	15	2 B49177	21K protein p2, mi
2	23	32.9	15	2 S21242	H-transferrin tw
3	23	32.9	16	2 S11760	figL protein - Cau
4	22	31.4	10	2 D33098	214K exoantigen (v
5	22	31.4	13	2 S36874	cytochrome P450 CM
6	22	31.4	16	2 S24667	protein-tyrosine k
7	21	30.0	12	2 S74196	3-hydroxy-3-methyl
8	21	30.0	13	2 A59491	epithelial dog all
9	21	30.0	14	2 S00150	ovostatin - duck (
10	21	30.0	15	2 B41436	ovostatin - green
11	21	30.0	16	2 A25213	antifreeze glycopr
12	20	28.6	13	2 A38929	glutathione peroxi
13	20	28.6	15	2 A45103	7 alpha-hydroxy-4-
14	20	28.6	15	2 B45115	peptidylprolyl iso
15	20	28.6	16	2 S01104	hypothetical prote
16	20	28.6	16	2 C61414	chymotrypsin (EC 3
17	19.5	27.9	14	4 S00843	hypothetical prote
18	19	27.1	11	2 C61497	seed protein ws-18
19	19	27.1	15	2 S05700	insulin-like growt
20	19	27.1	15	2 PNO052	pyruvate kinase (E
21	19	27.1	16	2 S68730	bleomycin-binding
22	18	25.7	10	2 PH1345	ig heavy chain DJ
23	18	25.7	11	4 PC2390	trichorizin I - fu
24	18	25.7	11	4 PC2391	trichorizin II - f
25	18	25.7	11	4 PC2392	trichorizin III -
26	18	25.7	11	4 PC2393	trichorizin IV - f
27	18	25.7	13	2 S09018	hemolytic protein
28	18	25.7	14	1 QMVHMM	mastoparan M - hor
29	18	25.7	14	1 QMVHP2	mastoparan C - Eur

30	18	25.7	14	2 JN0389	histamine-releasin
31	18	25.7	14	2 PA0094	hyocytamine (6s)-di
32	18	25.7	14	2 B56819	PS I complex subun
33	18	25.7	15	1 LFTWL	leu leader peptide
34	18	25.7	15	2 PA0106	protein QF200076 -
35	18	25.7	16	2 I75330	gene c-fms protein
36	18	25.7	16	2 I78533	gene agouti protein
37	18	25.7	16	2 S66613	protein p12E - Fri
38	17	24.3	7	2 PQ0727	H2 class I protein
39	17	24.3	9	4 S15594	orf 1 rara 5'-regi
40	17	24.3	10	2 JN0440	peptide-M4-(N-acet
41	17	24.3	10	2 C61033	ranatachykinin C -
42	17	24.3	11	4 I52708	ELAV-like neuronal
43	17	24.3	12	2 PA0019	acidic ribosomal P
44	17	24.3	13	2 S10562	zona pellucida-bin
45	17	24.3	13	2 JZVHP1	crabrolin - Europe
46	17	24.3	14	2 JN0390	histamine-releasin
47	17	24.3	14	2 B61235	fibroblast-activat
48	17	24.3	14	2 B60683	malate dehydrogena
49	17	24.3	14	2 F83754	hypothetical prote
50	17	24.3	15	2 A22789	platelet-derived g
51	17	24.3	15	2 PS0455	superoxide dismuta
52	17	24.3	15	2 I46309	voltage-dependent
53	17	24.3	16	2 S51610	hypothetical prote
54	17	24.3	16	2 A29520	amino-acid racemas
55	16	22.9	6	2 S66195	alcohol dehydrogen
56	16	22.9	9	2 B45796	dihydrolipoamide S
57	16	22.9	10	2 S65715	aryl hydrocarbon (
58	16	22.9	10	2 PC2171	triacylglycerol li
59	16	22.9	11	1 LFTWWE	probable trypsin lea
60	16	22.9	11	2 S66196	alcohol dehydrogen
61	16	22.9	11	2 S54347	tubulin beta chain
62	16	22.9	11	2 I77447	urinary protein -
63	16	22.9	12	2 S01122	photosystem II 3.7
64	16	22.9	12	2 S65136	kallikrein K2 - hu
65	16	22.9	12	2 PH1635	IG H chain V-D-J r
66	16	22.9	13	2 H85575	hypothetical prote
67	16	22.9	14	2 A60737	pollen allergen Lo
68	16	22.9	14	2 B20872	alpha-2-macroglobu
69	16	22.9	15	2 D46743	corneal keratan su
70	16	22.9	15	2 PT0097	glutathione peroxi
71	16	22.9	15	2 A49887	transcription fact
72	16	22.9	15	2 C43334	orf 3' to aadr -
73	16	22.9	15	2 S36897	ribosomal protein
74	16	22.9	15	2 S59489	steroid monooxygen
75	16	22.9	15	2 T09463	ribosomal protein
76	16	22.9	15	2 S54712	zein 2p22/6 protei
77	16	22.9	15	2 A36279	chemoattractant pr
78	16	22.9	15	4 I38336	hypothetical TEL/M
79	16	22.9	16	2 B60566	cytochrome P450m51
80	16	22.9	16	2 T09741	photosystem I chai
81	16	22.9	16	2 S02010	28K protein 4209 -
82	16	22.9	16	2 A61268	cytochrome P450-th
83	15	21.4	5	2 S55237	zinc-binding prote
84	15	21.4	8	2 S16324	hypothetical prote
85	15	21.4	9	2 S66419	tetrameric protein
86	15	21.4	9	2 PT0326	ig heavy chain CRD
87	15	21.4	9	2 B46250	alpha-adaptin - bo
88	15	21.4	9	2 S02384	probable membrane
89	15	21.4	9	2 D48186	ATPase R1 subunit
90	15	21.4	9	2 S13333	alpha/beta-gliadin
91	15	21.4	10	2 C39745	sphingomyelinase -
92	15	21.4	10	2 B45482	platelet activatin
93	15	21.4	10	2 S18396	probable glucose-6
94	15	21.4	10	2 S69159	cystathionine gamm
95	15	21.4	10	2 C26997	unspecific monooxy
96	15	21.4	11	2 S61797	T-cell-specific tr
97	15	21.4	11	2 I52304	gene rSTR4 protein
98	15	21.4	11	2 S41747	chaperonin 10 homo
99	15	21.4	12	2 S36899	ribosomal protein
100	15	21.4	12	2 S57570	T cell receptor V-

## ALIGNMENTS

## RESULT 1

B49177  
21K protein p2, mitochondrial - Crithidia fasciculata (fragment)  
C;Species: Crithidia fasciculata  
C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 09-Jul-2004  
C;Accession: B49177; PH1827  
R;Tittawella, I.

Exp. Cell Res. 206, 143-151, 1993  
A;Title: Identification of DNA-binding proteins in the parasitic protozoan Crithidia fasciculata  
A;Reference number: A49177; MUID:93245912; PMID:8482355  
A;Accession: B49177  
A;Molecule type: protein  
A;Residues: 1-15 <TIF>  
A;Cross-references: UNIPROT:Q9TWU3; UNIPARC:UPI000007BBF6  
A;Note: sequence extracted from NCBI backbone (NCBIP:131149)  
C;Comment: This protein binds with mitochondrial DNA.  
C;Keywords: DNA binding; mitochondrion

Query Match 34.3%; Score 24; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AAVALLPAVLLA 12  
|||:||||  
Db 2 AAGATMPAAAAA 13

## RESULT 2

S21242  
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - spinach mitochondrion (fragment)  
C;Species: mitochondrion Spinacia oleracea (spinach)  
C;Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: S21242

R;Hamasaur, B.; Glaser, E.  
Eur. J. Biochem. 205, 409-416, 1992  
A;Title: Plant mitochondrial F(0)F(1) ATP synthase. Identification of the individual subunits  
A;Reference number: S21204; MUID:92209531; PMID:1313368  
A;Accession: S21242

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-15 <HAM>  
A;Cross-references: UNIPROT:P80083; UNIPARC:UPI00001262CD  
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion

Query Match 32.9%; Score 23; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 2.3e+03;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AAVALLPAVLLA 12  
|||:||||  
Db 4 AAAAXAPSTPLA 15

## RESULT 3

S11760  
flgL protein - Caulobacter crescentus (fragment)  
C;Species: Caulobacter crescentus  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C;Accession: PQ0126; A25882; S11760  
R;Schoenlein, P.V.; Gallman, L.S.; Winkler, M.E.; Ely, B.  
Gene 93, 17-25, 1990

A;Title: Nucleotide sequence of the Caulobacter crescentus flaP and flbT genes and an analysis of their function  
A;Reference number: JQ0741; MUID:91033011; PMID:1699845  
A;Accession: PQ0126  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-16 <SCH>

A;Cross-references: UNIPROT:P18914; UNIPARC:UPI000016EAB1; GB:X15134; NID:g40418; PIDN:Q11760  
R;Minnich, S.A.; Newton, A.  
Proc. Natl. Acad. Sci. U.S.A. 84, 1142-1146, 1987

A;Title: Promoter mapping and cell cycle regulation of flagellin gene transcription in *Caulobacter crescentus*  
A;Reference number: A25882; MUID:87147229; PMID:3469658

A;Accession: A25882  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-12, 'V', 14-16 <MIN>  
A;Cross-references: UNIPARC:UPI000016EABE; GB:M15688; NID:g144267; PIDN:AAA23050.1; PID:Q11760  
C;Genetics:  
A;Gene: flgL

Query Match 32.9%; Score 23; DB 2; Length 16;  
Best Local Similarity 71.4%; Pred. No. 2.5e+03;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PAVLLAL 13  
|:||||  
Db 9 PGALLAL 15

## RESULT 4

D33098  
214K exoantigen (version 1) - malaria parasite (Plasmodium falciparum) (fragments)  
C;Species: Plasmodium falciparum  
C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C;Accession: D33098

R;Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A;Reference number: A33098  
A;Accession: D33098  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <NIC>  
A;Cross-references: UNIPARC:UPI000017B5E4

Query Match 31.4%; Score 22; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2.3e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 10 LLALLAP 16  
:|:|:  
Db 1 MLALLAP 7

## RESULT 5

S36874  
cytochrome P450 CMLb (EC 1.14.-.-) - crab-eating macaque (fragment)  
C;Species: Macaca fascicularis (crab-eating macaque)  
C;Date: 09-Jun-1994 #sequence\_revision 07-Nov-1997 #text\_change 09-Jul-2004  
C;Accession: S36874

R;Ohmori, S.; Horie, T.; Guengerich, F.P.; Kiuchi, M.; Kitada, M.  
Arch. Biochem. Biophys. 305, 405-413, 1993  
A;Title: Purification and characterization of two forms of hepatic microsomal cytochrome P450 CMLb  
A;Reference number: S36874; MUID:93384294; PMID:8373178  
A;Accession: S36874

A;Molecule type: protein  
A;Residues: 1-13 <OHM>  
A;Cross-references: UNIPROT:Q7M362; UNIPARC:UPI0000174CE1  
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology  
C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; liver; n

Query Match 31.4%; Score 22; DB 2; Length 13;  
Best Local Similarity 71.4%; Pred. No. 2.9e+03;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VLLALLA 15  
:|:|:  
Db 7 LLALLA 13

## RESULT 6

S24667  
protein-tyrosine kinase (EC 2.7.1.112) kit - mouse (fragment)  
C;Species: Mus musculus (house mouse)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 10, 2006, 17:02:31 ; Search time 85 Seconds  
(without alignments)  
174.121 Million cell updates/sec

Title: US-10-009-809-3

Perfect score: 70

Sequence: 1 AAVALLPAVALLALLAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 10172

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	41.4	14	2	Q6SEH1_9TELE
2	27	38.6	16	2	Q3YNF0_DROME
3	26	37.1	10	2	Q9H3R9_HUMAN
4	26	37.1	14	2	Q6GWV6_SHEEP
5	26	37.1	15	2	Q05694_MOUSE
6	26	37.1	16	2	Q7YJZ8_9FABA
7	26	37.1	16	2	Q9JHM3_RAT
8	25	35.7	10	1	TEMK_RANTE
9	25	35.7	10	2	Q5TKQ9_HUMAN
10	25	35.7	12	2	Q96PH0_HUMAN
11	25	35.7	14	2	Q6SEH0_9TELE
12	24	34.3	15	1	UC30_MAIZE
13	24	34.3	15	2	Q9TWU3_CRIFA
14	23	32.9	10	2	Q39949_9FLAV
15	23	32.9	10	2	Q39958_9FLAV
16	23	32.9	10	2	Q77VV7_9FLAV
17	23	32.9	10	2	Q77VV8_9FLAV
18	23	32.9	10	2	Q77ZJ1_9FLAV
19	23	32.9	10	2	Q77ZJ2_9FLAV
20	23	32.9	10	2	Q77ZJ3_9FLAV
21	23	32.9	10	2	Q77ZJ4_9FLAV
22	23	32.9	10	2	Q9W910_9FLAV
23	23	32.9	13	2	Q6T675_PAPAN
24	23	32.9	15	1	ATPBM_SF1OL
25	23	32.9	15	2	Q3YNF1_DROME
26	23	32.9	15	2	Q6GWV7_BOVIN
27	23	32.9	15	2	Q9TRN7_PIG
28	23	32.9	15	2	Q85713_9RETR
29	22	31.4	13	1	TE1LLA_RANLU
30	22	31.4	13	2	Q7M362_MACFA
31	22	31.4	13	2	Q53729_COXBU

32	22	31.4	14	2	Q5GK31_COXBU
33	22	31.4	14	2	Q5GK71_COXBU
34	22	31.4	15	1	PH3_PRUSE
35	22	31.4	15	2	Q2QHF8_SALET
36	22	31.4	15	2	Q5GK63_COXBU
37	22	31.4	16	2	Q4PZR8_9DIPS
38	22	31.4	16	2	Q4PZR9_VIBAC
39	22	31.4	16	2	Q4PZS0_9DIPS
40	22	31.4	16	2	Q570K0_ARATH
41	22	31.4	16	2	Q8UUE1_MEGTE
42	22	31.4	16	2	Q8UUE2_MEGPR
43	22	31.4	16	2	Q8UUE3_MEGLA
44	22	31.4	16	2	Q8UUE4_MEGRE
45	22	31.4	16	2	Q8UUE5_MEGFR
46	22	31.4	16	2	Q8UUE6_MEGFR
47	22	31.4	16	2	Q8UUE7_9GALL
48	22	31.4	16	2	Q8UUE8_MACML
49	22	31.4	16	2	Q8UUE9_9GALL
50	22	31.4	16	2	Q8UUF0_LEIOC
51	22	31.4	16	2	Q8UUF2_AEPAR
52	22	31.4	16	2	Q8UUF3_ALELA
53	21	30.0	11	2	Q84247_POVEK
54	21	30.0	13	2	P84494_CANPA
55	21	30.0	14	2	Q9MQQ3_PODCU
56	21	30.0	14	2	Q6UBES_BACFR
57	21	30.0	14	2	Q7LZ22_ANAPL
58	21	30.0	15	2	Q9UMT6_HUMAN
59	21	30.0	16	1	ANP8_ELEGR
60	21	30.0	16	2	Q4PZL9_9CARY
61	21	30.0	16	2	Q4PZM0_9CARY
62	21	30.0	16	2	Q8UUF4_NUMME
63	21	30.0	16	2	Q8UUF5_ALECH
64	21	30.0	16	2	Q8UUF6_PAVCR
65	21	30.0	16	2	Q8UUF7_9GALL
66	21	30.0	16	2	Q8UUF8_9GALL
67	20	28.6	9	2	Q15892_HUMAN
68	20	28.6	10	1	PAP1_PARMA
69	20	28.6	11	2	Q9TQB3_HUMAN
70	20	28.6	12	1	AMP1_PHYHY
71	20	28.6	12	2	Q2PCQ1_9FABA
72	20	28.6	12	2	Q9EQV3_MOUSE
73	20	28.6	13	2	Q16007_HUMAN
74	20	28.6	13	2	Q7M355_SHEEP
75	20	28.6	13	2	Q310N5_STAAU
76	20	28.6	13	2	Q9WMG5_SIGMA
77	20	28.6	13	2	Q9PWP4_DISMA
78	20	28.6	14	1	BGAT_MOUSE
79	20	28.6	14	2	Q3T4E7_RHIOR
80	20	28.6	14	2	Q2PRV9_9LAMI
81	20	28.6	14	2	Q617F6_9TELE
82	20	28.6	15	1	CWP07_DAUCA
83	20	28.6	15	2	Q27265_9TRYP
84	20	28.6	15	2	Q4PKZ5_9LAMI
85	20	28.6	15	2	Q4PKZ8_GRANE
86	20	28.6	15	2	Q4PZM4_9LAMI
87	20	28.6	15	2	Q4PZM6_ABUTH
88	20	28.6	15	2	Q4PZN9_9LAMI
89	20	28.6	15	2	Q4PZP0_GLEHE
90	20	28.6	15	2	Q4PZP6_9LAMI
91	20	28.6	15	2	Q4PZP7_9LAMI
92	20	28.6	15	2	Q8SLF5_9ASTR
93	20	28.6	15	2	Q8SLG7_9ASTR
94	20	28.6	15	2	Q9RS65_STRCO
95	20	28.6	15	2	Q9Q045_SIVCZ
96	20	28.6	16	2	Q4PKZ7_DATST
97	20	28.6	16	2	Q4PKZ9_ACENE
98	20	28.6	16	2	Q4PZL7_9ERIC
99	20	28.6	16	2	Q4PZM1_PHLDV
100	20	28.6	16	2	Q4PZM3_9POAL

ALIGNMENTS

```
RESULT 1
Q6SEH1_9TELE PRELIMINARY; PRT; 14 AA.
AC Q6SEH1;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Recombination-activating protein 1 (Fragment).
GN Names=RAG1;
OS Novumbra hubbsi.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Esociformes;
OC Uridae; Novumbra.
OX NCBI_TaxID=75937;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lopez A., Grande T., Laten H.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AY459525; AAS66762.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1462 MW; 2F36760EF77E57C7 CRC64;

Query Match 41.4%; Score 29; DB 2; Length 14;
Best Local Similarity 63.6%; Pred. No. 2.9e+03;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 VALLPAVLALL 13
DB 3 VGLHPAVCLAI 13

RESULT 2
Q3YNF0_DROME PRELIMINARY; PRT; 16 AA.
AC Q3YNF0;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE C88095 (Fragment).
GN Name=scb;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Brown R.P., Feder M.E.;
RL STRAIN=Oregon R;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: DQ017403; AAY82185.1; -; Genomic_DNA.
DR FlyBase; FBgn0003328; scb.
FT NON_TER 16
FT NON_TER 16
SQ SEQUENCE 16 AA; 1835 MW; 10965495A381085E CRC64;

Query Match 38.6%; Score 27; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 6.6e+03;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAVALLPAVLALL 14
DB 3 AESTMPHFVCLAI 16

RESULT 3
Q9H3R9_HUMAN PRELIMINARY; PRT; 10 AA.
AC Q9H3R9;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Deoxyribonuclease II (Fragment).
GN Name=DNASE2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yasuda T.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: AB031422; BAB20386.1; -; Genomic_DNA.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1067 MW; 3D5514DD7272737 CRC64;

Query Match 37.1%; Score 26; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.2e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 LLPAVLLALL 14
DB 1 MIPLLLALL 10

RESULT 4
Q6GWV6_SHEEP PRELIMINARY; PRT; 14 AA.
AC Q6GWV6;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Interleukin 8 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Meade K.G., Fitzgerald D.C., Murphy E.P., Baird A.W., MacHugh D.E.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: AY627309; AAT47551.1; -; Genomic_DNA.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1449 MW; D972E93C487C14C2 CRC64;

Query Match 37.1%; Score 26; DB 2; Length 14;
Best Local Similarity 77.8%; Pred. No. 8.3e+03;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AVALLPAVL 10
DB 6 AVALLAAFL 14

RESULT 5
Q05694_MOUSE PRELIMINARY; PRT; 15 AA.
ID Q05694_MOUSE
```

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OM protein - protein search, using sw model

Run on: July 10, 2006, 17:04:43 ; Search time 80 Seconds  
(without alignments)  
148.595 Million cell updates/sec

Title: US-10-009-809-7

Perfect score: 127

Sequence: 1 AAVALLPAVLLALLAPKNLKECGLY 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1035424

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A\_Geneseq\_8.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127	100.0	26	AAV72151	Succinyl
2	127	100.0	26	AAV72153	Anti-alle
3	127	100.0	26	AAV72139	Anti-alle
4	127	100.0	26	AAE26158	Galphai3
5	127	100.0	26	AAE26154	Peptide 2
6	127	100.0	26	AAE26156	Peptide 2
7	122	95.1	26	AAE26141	Galphai3
8	121	95.3	26	AAE26142	Galphai3
9	121	95.3	26	AAE26145	Galphai3
10	121	95.3	26	AAE26137	Galphai3
11	120	94.5	26	AAV72144	Modified
12	120	94.5	26	AAE26144	Galphai3
13	120	94.5	26	AAE26148	Galphai3
14	119	93.7	26	AAE26147	Galphai3
15	119	93.7	26	AAE26143	Galphai3
16	118	92.9	26	AAE26139	Galphai3
17	117	92.1	26	AAV72149	Anti-alle
18	117	92.1	26	AAE26138	Galphai3
19	117	92.1	26	AAE26146	Galphai3
20	114	89.8	26	AAV72152	Succinyl
21	114	89.8	26	AAV72142	Anti-alle
22	114	89.8	26	AAE26155	Peptide 5
23	98.5	77.6	23	AAV72147	Anti-alle

24	91.5	72.0	23	4	AAV72148	Anti-alle
25	80	63.0	25	2	AAW53778	KARPOSI S
26	79	62.2	22	3	AAV67957	KARPOSI S
27	77	60.6	26	9	ADZ68077	MAP Kinas
28	75	59.1	17	3	AAV67960	KARPOSI S
29	75	59.1	19	3	AAV67955	KARPOSI S
30	75	59.1	20	3	AAV67962	KARPOSI S
31	75	59.1	22	3	AAV67958	KARPOSI S
32	74	58.3	26	2	AAW87635	BAM-SP CO
33	74	58.3	26	4	AAU03158	Peptide S
34	74	58.3	26	8	ADQ91933	Kaposi fi
35	74	58.3	26	9	AE848524	Kaposi fi
36	74	58.3	26	9	AE05504	Kaposi fi
37	73	57.5	24	2	AAW53779	KARPOSI S
38	72	56.7	22	10	AAE92006	Polyynucle
39	72	56.7	22	10	AAE92080	Polyynucle
40	72	56.7	22	10	AAE92080	Polyynucle
41	70	55.1	16	2	AAW87629	Signal pe
42	70	55.1	16	2	AAW37753	Chimeric
43	70	55.1	16	2	AAW56394	MEM polyp
44	70	55.1	16	2	AAW48689	Signal pe
45	70	55.1	16	2	AAW53769	KARPOSI S
46	70	55.1	16	2	AAV13506	Signal se
47	70	55.1	16	3	AAV67954	KARPOSI S
48	70	55.1	16	3	AAV55815	Fibroblas
49	70	55.1	16	4	AAE02979	Hydrophob
50	70	55.1	16	4	AAU97005	CCAAT enh
51	70	55.1	16	4	AAE11949	Membrane
52	70	55.1	16	4	AAU03154	Peptide K
53	70	55.1	16	4	AAV72476	Kaposi fi
54	70	55.1	16	5	ABG78989	Cell pene
55	70	55.1	16	5	AAU10399	Membrane
56	70	55.1	16	5	AAE15613	Kaposi's
57	70	55.1	16	5	AAU78349	Signal se
58	70	55.1	16	5	AAE26128	Kaposi fi
59	70	55.1	16	5	ABG75507	Signal-se
60	70	55.1	16	5	AB881177	Signal se
61	70	55.1	16	6	AAE23686	Fluoresce
62	70	55.1	16	6	ABR84444	K-FGF sig
63	70	55.1	16	6	AAE33897	Kaposi's
64	70	55.1	16	6	ABU09984	Kaposi's
65	70	55.1	16	7	ADC22454	Protein-d
66	70	55.1	16	7	ADF78064	Human mem
67	70	55.1	16	7	ADG28017	Kaposi FG
68	70	55.1	16	7	ADH76184	Transduct
69	70	55.1	16	7	ADK11581	Taxoid ca
70	70	55.1	16	7	ADL88653	MPS (Kapo
71	70	55.1	16	8	ADG73832	Peptide d
72	70	55.1	16	8	ADH58870	Glutathio
73	70	55.1	16	8	ADJ78875	N-termina
74	70	55.1	16	8	ADL14686	Cardiant
75	70	55.1	16	8	ADK15574	Membrane
76	70	55.1	16	8	ADO26466	Kaposi's
77	70	55.1	16	8	ADM97016	Botulinum
78	70	55.1	16	8	ADO25265	Signal se
79	70	55.1	16	8	ADP08148	Small int
80	70	55.1	16	8	ADP08145	Small int
81	70	55.1	16	8	ADP08145	Human her
82	70	55.1	16	8	ADG60179	Heat choc
83	70	55.1	16	8	ADR31572	Membrane
84	70	55.1	16	8	ADR82252	MUCI-PDZ
85	70	55.1	16	8	ADT61097	Novel int
86	70	55.1	16	8	ADU07192	Membrane
87	70	55.1	16	8	ADT61891	Human mem
88	70	55.1	16	8	ADT86673	Membrane
89	70	55.1	16	8	ADU67511	Membrane
90	70	55.1	16	8	ADU26590	Cell perm
91	70	55.1	16	8	AE819669	Novel gen
92	70	55.1	16	9	ADW25982	Membrane
93	70	55.1	16	9	ADW81340	Intrabody
94	70	55.1	16	9	ADW86632	Membrane
95	70	55.1	16	9	ADY32269	Novel can
96	70	55.1	16	9	ADY38682	Novel pro

97	70	55.1	16	9	AD264558	Kaposi's
98	70	55.1	16	9	AD268062	Kaposi's
99	70	55.1	16	9	AD269395	HSP20 tra
100	70	55.1	16	9	AE98089	Signal se

## ALIGNMENTS

RESULT 1	
AA72151	
ID	AA72151 standard; peptide; 26 AA.
XX	
AC	AA72151;
XX	
DT	24-APR-2001 (first entry)
XX	
DE	Succinylated anti-allergic peptide 2.
XX	
KW	Anti-allergic peptide; therapeutic; migraine; psoriasis; asthma; multiple sclerosis; nasal allergy; mast cell degranulation; histamine; allergy; eye; skin; acute urticaria; interstitial cystitis; vasotropic; psychogenic; bowel disease; dermatological; antiinflammatory; G alpha i3; neuroprotective; antipsoriatic; Kaposi fibroblast growth factor; fusion peptide; exocytosis.
KW	
KW	
XX	
OS	Synthetic.
XX	
XX	
FH	Key
XX	Location/Qualifiers
FT	1..16
FT	/label= Signal peptide
FT	/note= Signal sequence of Kaposi fibroblast growth factor; this region is referred in claim 48"
FT	1
FT	Modified-site
FT	/note= "Succinylated alanine"
FT	17..26
FT	Peptide
FT	/label= G_alpha i3_peptide
FT	/note= "Corresponds to C-terminal sequence of G_alpha i3"
XX	
WO	WO200078346-A1.
PN	
XX	
PD	28-DEC-2000.
XX	
PF	14-JUN-2000; 2000WO-IL000346.
XX	
PR	17-JUN-1999; 99IL-00130526.
XX	
PA	(ALLE-) ALLERGENE LTD.
XX	
PI	Eisenberg R, Raz T;
XX	
XX	WPI; 2001-080758/09.
DR	
PT	Novel anti-allergic agents for treating allergic conditions such as allergic reactions in eye, skin, nasal allergy, asthma, migraines, has peptides for cell penetration and reducing mast cell degranulation.
PT	
XX	
PS	Claim 29; Page 44; 63pp; English.
XX	
CC	The present sequence is succinylated anti-allergic peptide 2 consisting of a signal sequence of Kaposi fibroblast growth factor, linked to the C-terminal G_alpha i3 sequence. This C-terminal G_alpha i3 appears to mediate the peptidergic pathway leading to exocytosis in mast cells. A succinyl residue is added to the N-terminus of peptide 2 (AA72139), for improving the peptide solubility. The invention relates to therapeutic complex molecules which are useful as anti-allergic agents. These anti-allergic agents are useful for treating allergic conditions such as nasal allergy allergic reaction in the eye or skin, acute urticaria, psoriasis, psychogenic or allergic asthma, interstitial cystitis, bowel diseases, migraines and multiple sclerosis. The therapeutic complex is highly specific, direct and provides targeted treatment of allergies and related inflammatory conditions. It comprises molecules having at least a first segment i.e. a signal peptide which is competent for the

CC importation of the complex into the mast cells, and a second segment  
CC which is having the anti-allergic effect is able to block or  
CC significantly reduce the G protein-mediated contribution to mast cell  
CC degranulation and in turn the release of histamine. The invention also  
CC discloses methods for preventing and treating allergies  
XX  
SQ Sequence 26 AA;  
  
Query Match 100.0%; Score 127; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2	
AA72153	AA72153 standard; peptide; 26 AA.
XX	XX
XX	AA72153;
XX	XX
XX	24-APR-2001 (first entry)
XX	XX
XX	Anti-allergic cyclic peptide 2.
XX	XX
XX	Anti-allergic peptide; therapeutic; migraine; psoriasis; asthma;
KW	multiple sclerosis; nasal allergy; mast cell degranulation; histamine;
KW	allergy; eye; skin; acute urticaria; interstitial cystitis; vasotropic;
KW	psychogenic; bowel disease; dermatological; antiinflammatory; G alpha13;
KW	neuroprotective; antipsoriatic; Kaposi fibroblast growth factor; cyclic;
XX	fusion peptide; exocytosis.
XX	XX
OS	Synthetic.
XX	XX
FH	Key
XX	Location/Qualifiers
FT	Peptide
FT	1. .16
FT	/label= Signal_peptide
FT	/note= "Signal sequence of Kaposi fibroblast growth
FT	factor; this region is referred in clalm 48"
FT	17. .26
FT	Peptide
FT	/label= G alpha13_peptide
FT	/note= "Corresponds to C-terminal sequence of G alpha13"
FT	17
FT	Modified-site
FT	/note= "The side chain of Lys residue forms a cyclic bond
FT	with Tyr found at the C-terminal end"
FT	26
FT	Modified-site
FT	/note= "The C-terminal end of the peptide forms a cyclic
FT	bond with side chain of Lys at position 17"
XX	XX
XX	WO200078346-A1.
XX	XX
XX	28-DEC-2000.
XX	XX
XX	14-JUN-2000; 2000WO-IL000346.
PF	XX
XX	17-JUN-1999; 99IL-00130526.
XX	XX
XX	(ALLE-) ALLERGENE LTD.
PA	XX
XX	Eisenberg R, Raz T;
PI	XX
XX	XX
XX	WPI; 2001-080758/09.
DR	XX
XX	XX
XX	Novel anti-allergic agents for treating allergic conditions such as
PT	allergic reactions in eye, skin, nasal allergy, asthma, migraines, has
PT	peptides for cell penetration and reducing mast cell degranulation.
XX	XX
XX	Example 3; Page 24; 63pp; English.
XX	XX
XX	The present sequence is cyclic anti-allergic peptide 2 consisting of a
CC	signal sequence of Kaposi fibroblast growth factor, linked to the C-
CC	



GenCore version 5.1.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 17:05:16 ; Search time 24 Seconds  
(without alignments)  
94.825 Million cell updates/sec

Title: US-10-009-809-7

Perfect score: 127  
Sequence: 1 AAVALLPAVLLALLAPKNLKECGLY 26

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 315764

Minimum DB seq length: 0  
Maximum DB seq length: 26

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents\_AA.\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCITUS\_COMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	63.0	25	2	US-09-230-548-20
2	74	58.3	26	1	US-08-258-852-9
3	74	58.3	26	2	US-09-170-754B-9
4	74	58.3	26	2	US-09-450-071A-9
5	74	58.3	26	2	US-09-997-465B-1
6	74	58.3	26	5	PCT-US95-07539-9
7	73	57.5	24	2	US-09-230-548-21
8	70	55.1	16	1	US-08-642-493-1
9	70	55.1	16	1	US-08-258-852-5
10	70	55.1	16	1	US-08-928-958-4
11	70	55.1	16	1	US-09-072-429-4
12	70	55.1	16	2	US-08-964-302A-3
13	70	55.1	16	2	US-09-170-754B-5
14	70	55.1	16	2	US-09-441-416A-3
15	70	55.1	16	2	US-09-411-706-1
16	70	55.1	16	2	US-09-230-548-19
17	70	55.1	16	2	US-09-450-071A-5
18	70	55.1	16	2	US-09-935-032-1
19	70	55.1	16	2	US-10-083-889-7
20	70	55.1	16	2	US-10-116-288A-23
21	70	55.1	16	2	US-10-144-549-18
22	70	55.1	16	2	PCT-US95-07539-5
23	70	55.1	20	2	US-09-623-548A-1058
24	70	55.1	20	2	US-09-623-548A-1060
25	70	55.1	20	2	US-09-657-276-1058
26	70	55.1	20	2	US-09-657-276-1060

27	70	55.1	20	2	US-09-657-276-1060	Sequence 1060, Ap
28	70	55.1	26	1	US-08-258-852-1	Sequence 1, Appli
29	70	55.1	26	1	US-08-258-852-3	Sequence 3, Appli
30	70	55.1	26	1	US-08-258-852-8	Sequence 8, Appli
31	70	55.1	26	1	US-08-928-958-5	Sequence 5, Appli
32	70	55.1	26	1	US-09-072-429-5	Sequence 5, Appli
33	70	55.1	26	2	US-09-170-754B-1	Sequence 1, Appli
34	70	55.1	26	2	US-09-170-754B-3	Sequence 3, Appli
35	70	55.1	26	2	US-09-170-754B-8	Sequence 8, Appli
36	70	55.1	26	2	US-09-450-071A-1	Sequence 1, Appli
37	70	55.1	26	2	US-09-450-071A-3	Sequence 3, Appli
38	70	55.1	26	2	US-09-450-071A-8	Sequence 8, Appli
39	70	55.1	26	2	US-09-450-071A-13	Sequence 13, Appli
40	70	55.1	26	2	US-09-998-350-18	Sequence 18, Appli
41	70	55.1	26	2	US-09-998-350-19	Sequence 19, Appli
42	70	55.1	26	5	PCT-US95-07539-1	Sequence 1, Appli
43	70	55.1	26	5	PCT-US95-07539-3	Sequence 3, Appli
44	70	55.1	26	5	PCT-US95-07539-8	Sequence 8, Appli
45	67	52.8	26	1	US-08-928-958-2	Sequence 2, Appli
46	67	52.8	26	1	US-09-072-429-2	Sequence 2, Appli
47	63	49.6	15	1	US-08-928-958-8	Sequence 8, Appli
48	63	49.6	15	1	US-09-072-429-8	Sequence 8, Appli
49	63	49.6	16	2	US-09-720-039-1	Sequence 1, Appli
50	63	49.6	17	2	US-10-393-903-1	Sequence 1, Appli
51	63	49.6	26	2	US-09-720-039-3	Sequence 3, Appli
52	57	44.9	11	2	US-09-489-156-39	Sequence 39, Appli
53	57	44.9	13	2	US-09-489-156-18	Sequence 18, Appli
54	50	39.4	10	1	US-08-019-073-19	Sequence 19, Appli
55	50	39.4	10	1	US-08-429-964-50	Sequence 50, Appli
56	50	39.4	10	5	PCT-US93-08062-50	Sequence 50, Appli
57	50	39.4	10	5	PCT-US94-01768-19	Sequence 19, Appli
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; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 2200.021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 9:
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; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
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Best Local Similarity 94.4%; Pred. No. 8e-05;
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; APPLICANT: Lin, Yao-zhong
; APPLICANT: Hawiger, Jack J.
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; TITLE OF INVENTION: BIOLOGICALLY ACTIVE MOLECULES INTO CELLS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: 127 Peachtree Street, N.E.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/09/170,754B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/258,852
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 2200.021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 9:
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; LENGTH: 26 amino acids
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; TOPOLOGY: linear
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Best Local Similarity 94.4%; Pred. No. 8e-05;
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GenCore version 5.1.9  
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Title: US-10-009-809-7

Perfect score: 127

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Minimum DB seq length: 0

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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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GenCore version 5.1.9  
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63	28	22.0	15	7	US-11-140-487A-2179	Sequence 2179, Ap
64	28	22.0	15	7	US-11-140-487A-2236	Sequence 2236, Ap
65	28	22.0	17	7	US-11-140-487A-2271	Sequence 2271, Ap
66	28	22.0	22	6	US-10-449-902-36488	Sequence 36488, A
67	28	22.0	25	7	US-11-154-977-79	Sequence 1599, Ap
68	28	22.0	26	7	US-11-140-487A-1389	Sequence 1389, Ap
69	27	21.3	9	7	US-11-340-431-34	Sequence 34, Appli
70	27	21.3	9	7	US-11-340-431-35	Sequence 35, Appli
71	27	21.3	9	7	US-11-340-431-58	Sequence 58, Appli
72	27	21.3	9	7	US-11-340-431-255	Sequence 255, App
73	27	21.3	9	7	US-11-340-431-261	Sequence 261, App
74	27	21.3	9	7	US-11-303-372-15	Sequence 15, Appli
75	27	21.3	11	7	US-11-303-372-73	Sequence 73, Appli
76	27	21.3	11	7	US-11-293-891-18	Sequence 18, Appli
77	27	21.3	11	7	US-11-303-372-1	Sequence 1, Appli
78	27	21.3	12	7	US-11-303-372-14	Sequence 14, Appli
79	27	21.3	12	7	US-11-303-372-72	Sequence 72, Appli
80	27	21.3	12	7	US-11-263-230-297	Sequence 297, App
81	27	21.3	12	7	US-11-259-133-110	Sequence 110, App
82	27	21.3	12	7	US-11-259-266-38	Sequence 38, Appli
83	27	21.3	12	7	US-11-259-267-38	Sequence 38, Appli
84	27	21.3	12	7	US-11-023-241-1	Sequence 1, Appli
85	27	21.3	12	7	US-10-953-613C-801	Sequence 801, App
86	27	21.3	13	6	US-11-303-372-6	Sequence 6, Appli
87	27	21.3	13	7	US-11-303-372-64	Sequence 64, Appli
88	27	21.3	13	7	US-11-270-295A-5	Sequence 5, Appli
89	27	21.3	16	7	US-11-303-372-5	Sequence 5, Appli
90	27	21.3	16	7	US-11-303-372-63	Sequence 63, Appli
91	27	21.3	16	7	US-11-303-372-23	Sequence 23, Appli
92	27	21.3	17	7	US-11-303-372-81	Sequence 81, Appli
93	27	21.3	17	7	US-11-340-431-1	Sequence 1, Appli
94	27	21.3	17	7	US-11-340-431-13	Sequence 13, Appli
95	27	21.3	17	6	US-10-521-319-17	Sequence 17, Appli
96	27	21.3	20	7	US-11-334-622-11	Sequence 11, Appli
97	27	21.3	21	7	US-11-134-871-1801	Sequence 1801, Ap
98	27	21.3	21	7		

99 27 21.3 22 6 US-10-503-836-6 Sequence 6, Appli  
100 27 21.3 22 7 US-11-154-977-143 Sequence 143, App

## ALIGNMENTS

RESULT 1  
US-11-214-588-23  
; Sequence 23, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 23  
; LENGTH: 26  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-214-588-23

Query Match 100.0%; Score 127; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVALPVLALLAPKNNLKECGLY 26  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 AAVALPVLALLAPKNNLKECGLY 26

RESULT 2  
US-11-214-588-24  
; Sequence 24, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 24  
; LENGTH: 26  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; NAME/KEY: BINDING  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: N-terminal amino acid is succinylated  
US-11-214-588-24

Query Match 100.0%; Score 127; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVALPVLALLAPKNNLKECGLY 26  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 AAVALPVLALLAPKNNLKECGLY 26

RESULT 3  
US-11-214-588-26  
; Sequence 26, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 26  
; LENGTH: 26  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; NAME/KEY: BINDING  
; LOCATION: (17)..(26)  
; OTHER INFORMATION: A bond exists between the side chain of K at position 17 and the  
; OTHER INFORMATION: c-terminus of the peptide  
US-11-214-588-26

Query Match 100.0%; Score 127; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVALPVLALLAPKNNLKECGLY 26  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 AAVALPVLALLAPKNNLKECGLY 26

RESULT 4  
US-11-214-588-29  
; Sequence 29, Application US/11214588  
; Publication No. US20060100141A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Ronit  
; TITLE OF INVENTION: ANTI-ALLERGIC COMPLEX MOLECULES  
; FILE REFERENCE: 85189-4799  
; CURRENT APPLICATION NUMBER: US/11/214,588  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US 10/465,826  
; PRIOR FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: PCT/IL01/01186  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 29  
; LENGTH: 26  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-214-588-29

Query Match 100.0%; Score 127; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 10, 2006, 17:05:11 ; Search time 22 Seconds  
(without alignments)  
113.711 Million cell updates/sec

Title: US-10-009-809-7

Perfect score: 127

Sequence: 1 AAVALLPAVILLALLAPKNLKECGLY 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 5210

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR\_80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	22.8	19	I53673	amyloid protein -
2	29	22.8	22	S29326	hypothetical prote
3	29	22.8	26	1 SREPT4	stp protein - phag
4	29	22.8	26	S5799	stp protein - phag
5	29	22.8	26	S5798	stp protein - phag
6	29	22.8	26	S5797	stp protein - phag
7	29	22.8	26	S5800	stp protein (varia
8	28.5	22.4	24	PH1336	Ig heavy chain DJ
9	28	22.0	23	B31657	major fecal allerg
10	27	21.3	18	A28060	elastase inhibitor
11	27	21.3	20	C60822	cytochrome P450 U
12	27	21.3	26	A23456	pepsin A (EC 3.4.2
13	26	20.5	13	S78519	ribosomal protein
14	26	20.5	20	S11471	25-hydroxyvitamin
15	26	20.5	20	S65746	hypothetical prote
16	26	20.5	22	B39138	dihydrolipoamide S
17	26	20.5	23	S34739	trans-cinnamate 4-
18	26	20.5	24	E20554	hemocyanin subunit
19	26	20.5	25	S26233	ribosomal protein
20	25.5	20.1	18	PH1350	Ig heavy chain DJ
21	25	19.7	21	S33979	testosterone 15alp
22	25	19.7	23	A31944	cytochrome P450NMA
23	25	19.7	24	T43971	CC-chemokine recep
24	24	18.9	13	PQ0445	urotensin II - lau
25	24	18.9	15	B49177	21K protein p2, mi
26	24	18.9	16	S24667	protein-tyrosine k
27	24	18.9	20	S16478	tray protein - Esc
28	24	18.9	22	A53630	anti-HIV antidioti
29	24	18.9	21	S07817	spike glycoprotein

30	24	18.9	24	154750	class II major his
31	24	18.9	24	T29626	hypothetical prote
32	24	18.9	26	S11629	elastin precursor
33	24	18.9	26	A57221	pilin, type IV - A
34	23	18.1	15	S21242	H+-transporting tw
35	23	18.1	16	S11760	figl protein - Cau
36	23	18.1	18	I52614	u-plasminogen acti
37	23	18.1	18	B32220	T-cell receptor de
38	23	18.1	19	I54264	rhodopsin single b
39	23	18.1	20	I38417	HLA-A11 - human (f
40	23	18.1	20	S38763	S-adenosyl-L-methi
41	23	18.1	21	A44139	RNA-polymerase-ass
42	23	18.1	23	B37843	vrg 18 protein - B
43	23	18.1	25	A32203	dihydrofolate redu
44	23	18.1	26	S16181	calpain (EC 3.4.22
45	22	17.3	5	S65726	hemoglobin, extrac
46	22	17.3	7	A11483	aspartate transami
47	22	17.3	10	D33098	214K exoantigen (v
48	22	17.3	13	S36874	cytochrome P450 CM
49	22	17.3	13	A38929	glutathione peroxi
50	22	17.3	17	A61557	major merozoite su
51	22	17.3	20	A60822	cytochrome P450 PB
52	22	17.3	20	S21737	coumarin 7-monoxy
53	22	17.3	20	A14344	alanine transamina
54	22	17.3	20	I38418	HLA-A2 - human (fr
55	22	17.3	20	S50175	kallikrein (PK-120
56	22	17.3	20	T48881	leader peptide (im
57	22	17.3	20	S10680	probable 7-ethoxyc
58	22	17.3	21	S09517	prolamin - sorghum
59	22	17.3	21	A60225	pyruvate dehydroge
60	22	17.3	22	S17514	70K protein - rabb
61	22	17.3	23	I55406	nicotinic acetylch
62	22	17.3	24	E39690	neural cell adhesi
63	22	17.3	24	A60484	photosystem II oxy
64	22	17.3	24	S05410	glucose 1-dehydrog
65	22	17.3	24	S70333	endosperm protein,
66	22	17.3	24	PX0038	methemoglobin redu
67	22	17.3	26	S36921	NADH2 dehydrogenas
68	22	17.3	26	E27011	MHC class II-assoc
69	22	17.3	26	H30667	hypothetical prote
70	22	17.3	26	C85648	hypothetical prote
71	21.5	16.9	16	S01104	hypothetical prote
72	21	16.5	12	S74196	3-hydroxy-3-methyl
73	21	16.5	13	S09395	hypothetical prote
74	21	16.5	13	A59491	epithelial dog all
75	21	16.5	14	S00150	ovostatin - duck (
76	21	16.5	15	B41436	ovostatin - green
77	21	16.5	16	A25213	antifreeze glycopr
78	21	16.5	18	A28027	protein P2 - curle
79	21	16.5	19	B25213	antifreeze glycopr
80	21	16.5	20	A54083	p190/210, fatty ac
81	21	16.5	20	PL0192	Ig lambda 2 chain
82	21	16.5	20	I54283	arylsulfatase A -
83	21	16.5	20	A61323	histone H1.0a - bo
84	21	16.5	20	A41717	P100 protein - rat
85	21	16.5	20	C49753	hypothetical prote
86	21	16.5	20	A54077	cytochrome bs58 -
87	21	16.5	21	S21772	lipoxigenase (EC 1
88	21	16.5	21	S33287	DNA polymerase - T
89	21	16.5	21	S38739	lipid transfer pro
90	21	16.5	22	PQ0697	hemagglutinin (imp
91	21	16.5	23	S11210	collagen alpha 2(I
92	21	16.5	23	T17073	NADH2 dehydrogenas
93	21	16.5	24	B23317	threonine ammonia-
94	21	16.5	24	A43941	extracellular mura
95	21	16.5	24	S13566	matrix protein - h
96	21	16.5	24	A36912	hypothetical prote
97	21	16.5	24	S10682	cytochrome P450 is
98	21	16.5	25	S61504	62K protein - Euba
99	21	16.5	25	F84066	hypothetical prote
100	21	16.5	26	S59906	gamma-glutamyl tra

ALIGNMENTS

RESULT 1  
153673  
amyloid protein - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 13-Aug-1999  
C:Accession: I53673  
R:Chernak, J.M.  
Gene 133, 255-260, 1993  
A:Title: Structural features of the 5' upstream regulatory region of the gene encoding x  
A:Reference number: I53673; MUID:94040820; PMID:8224912  
A:Accession: I53673  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-19 <RES>  
A:Cross-references: UNIPARC:UPI00000003B7; GB:L11926; NID:g949984; PIDN:AAA74458.1; PID:  
C:Genetics:  
A:Gene: APP  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

Query Match 22.8%; Score 29; DB 2; Length 19;  
Best Local Similarity 54.5%; Pred. No. 9.3e+02;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LLPAVLLALLA 15  
:|:|:|  
Db 1 MLPSSLALLA 11

RESULT 2  
S29326  
hypotheical protein 22, psba 5'-region - Japanese black pine chloroplast  
C:Species: chloroplast Pinus thunbergiana (Japanese black pine)  
C:Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004  
C:Accession: S29326; T07427  
R:Tsudzuki, J.; Nakashima, K.; Tsudzuki, T.; Hiratsuka, J.; Shibata, M.; Wakasugi, T.; S  
Mol. Gen. Genet. 232, 206-214, 1992  
A:Title: Chloroplast DNA of black pine retains a residual inverted repeat lacking rRNA g  
A:Reference number: S20449; MUID:92212283; PMID:1557027  
A:Accession: S29326  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-22 <TSU>  
A:Cross-references: UNIPROT:Q37112; UNIPARC:UPI0000092202; EMBL:D11467; NID:g344007; PID  
R:Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiyura, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994  
A:Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome  
A:Reference number: Z16030; MUID:95024047; PMID:7937893  
A:Accession: T07427  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-22 <WAK>  
A:Cross-references: UNIPARC:UPI0000092202; EMBL:D17510; NID:g529643; PIDN:BAA04307.1; PI  
C:Genetics:  
A:Genome: chloroplast  
C:Keywords: chloroplast

Query Match 22.8%; Score 29; DB 2; Length 22;  
Best Local Similarity 80.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 22 ECGLY 26  
|:|:|  
Db 11 ECGIY 15

RESULT 3  
STBPT4  
stp protein - phase T4  
C:Species: phase T4  
A:Note: host Escherichia coli

C:Date: 30-Sep-1990 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004  
C:Accession: S55796; S01869; S49926  
R:Penner, M.; Morad, I.; Snyder, L.; Kaufmann, G.  
J. Mol. Biol. 249, 857-868, 1995  
A:Title: Phase T4-coded Stp: double-edged effector of coupled DNA and tRNA-restriction s  
A:Reference number: S55796; MUID:95311310; PMID:7791212  
A:Accession: S55796  
A:Molecule type: DNA  
A:Residues: 1-26 <PEN>  
A:Cross-references: UNIPROT:P18788; UNIPARC:UPI000005CBF4; EMBL:Z46874; NID:g599667; PID:  
A:Note: this is a revision to the sequence from reference S01711  
R:Chapman, D.; Morad, I.; Kaufmann, G.; Gait, M.J.; Jorissen, L.; Snyder, L.  
J. Mol. Biol. 199, 373-377, 1988  
A:Title: Nucleotide and deduced amino acid sequence of stp: the bacteriophage T4 antio  
A:Reference number: S01711; MUID:88172481; PMID:3280805  
A:Accession: S01869  
A:Molecule type: DNA  
A:Residues: 1-20 'RLRTPVRKI' <CHA>  
A:Cross-references: UNIPARC:UPI0000174B95  
A:Note: this sequence has been revised in reference S55796  
C:Genetics:  
A:Gene: stp  
A:Map position: 162-164  
C:Superfamily: phase T4 stp protein

Query Match 22.8%; Score 29; DB 1; Length 26;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 17 KNNLKECGLY 26  
:|:|:|  
Db 14 RNNLKTGVF 23

RESULT 4  
S55799  
stp protein - phase LZ5  
C:Species: phase LZ5  
C:Date: 08-Jul-1995 #sequence\_revision 18-Jul-1997 #text\_change 20-Sep-1999  
A:Accession: S55799; S49923  
R:Penner, M.; Morad, I.; Snyder, L.; Kaufmann, G.  
J. Mol. Biol. 249, 857-868, 1995  
A:Title: Phase T4-coded Stp: double-edged effector of coupled DNA and tRNA-restriction s  
A:Reference number: S55796; MUID:95311310; PMID:7791212  
A:Accession: S55799  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-26 <PEN>  
A:Cross-references: UNIPARC:UPI000005CBF4; EMBL:Z46876; NID:g599661; PIDN:CAA86956.1; PI  
C:Genetics:  
A:Gene: stp  
A:Superfamily: phase T4 stp protein

Query Match 22.8%; Score 29; DB 2; Length 26;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 17 KNNLKECGLY 26  
:|:|:|  
Db 14 RNNLKTGVF 23

RESULT 5  
S55798  
stp protein - phase TuiB  
C:Species: phase TuiB  
C:Date: 08-Jul-1995 #sequence\_revision 18-Jul-1997 #text\_change 20-Sep-1999  
A:Accession: S55798; S49990  
R:Penner, M.; Morad, I.; Snyder, L.; Kaufmann, G.  
J. Mol. Biol. 249, 857-868, 1995  
A:Title: Phase T4-coded Stp: double-edged effector of coupled DNA and tRNA-restriction s  
A:Reference number: S55796; MUID:95311310; PMID:7791212  
A:Accession: S55798



GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on:

July 10, 2006, 17:05:01 ; Search time 85 Seconds  
(without alignments)  
282.946 Million cell updates/sec

Title: US-10-009-809-7

Perfect score: 127

Sequence: 1 AAVALLPAVLLALLAPKNLKECGLY 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 25239

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt\_7.2.1\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	29.9	20	Q425N7	PLABE
2	37.5	29.5	18	Q9QWQ4	MOUSE
3	35	27.6	13	Q5D4Q9	agrobacteri
4	35	27.6	18	Q3SX59	HUMAN
5	34	26.8	23	Q87083	9ALPH
6	33	26.0	22	Q6SZK5	RHOFA
7	32	25.2	17	Q2WG84	HUMAN
8	32	25.2	24	Q9UMM9	HUMAN
9	32	25.2	24	Q7SCF5	NEUCR
10	31	24.4	21	Q9HD54	HUMAN
11	31	24.4	24	Q7Z5M2	HUMAN
12	30	23.6	13	Q9TKG6	9CHLO
13	30	23.6	20	Q9R595	9SYNE
14	30	23.6	24	Q9N685	STRPU
15	30	23.6	26	Q4H4Y8	9DEIO
16	30	23.6	26	Q8R2L8	MOUSE
17	29.5	23.2	19	Q9H2B3	HUMAN
18	29.5	23.2	21	Q6SIW7	SALNE
19	29.5	23.2	21	Q8GKW6	SALE
20	29.5	23.2	26	Q2QDB3	9VIRU
21	29.5	23.2	26	Q2QDB6	cauliflower
22	29.5	23.2	26	Q2QDB9	9VIRU
23	29.5	23.2	26	Q2QDC2	9VIRU
24	29.5	23.2	26	Q64FW9	9VIRU
25	29	22.8	13	Q9T4K3	9CHLO
26	29	22.8	13	Q9T4K4	9CHLO
27	29	22.8	13	Q9T4K5	9CHLO
28	29	22.8	13	Q9T4K6	9CHLO
29	29	22.8	13	Q9THS2	9CHLO
30	29	22.8	14	Q6SEH1	9TELE
31	29	22.8	18	Q52RG2	HUMAN

32	29	22.8	19	2	Q6LEE8	RAT
33	29	22.8	22	2	Q37112	PINTH
34	29	22.8	22	2	Q900A6	9HIV1
35	29	22.8	22	2	Q97064	9HIV1
36	29	22.8	24	2	Q7RS38	PLASMO
37	29	22.8	26	1	STP_BBLZ3	
38	29	22.8	26	1	STP_BPT25	
39	29	22.8	26	1	STP_BPT4	
40	29	22.8	26	1	Q38084	9CAUD
41	28.5	22.4	14	2	Q9OVF3	9MURI
42	28	22.0	16	2	Q4PZR8	9DIPS
43	28	22.0	16	2	Q4PZR9	9DIPS
44	28	22.0	16	2	Q4PZS0	9DIPS
45	28	22.0	16	2	Q7YJZ8	9FABA
46	28	22.0	18	2	Q8WN06	BOVIN
47	28	22.0	19	2	Q97584	MACMU
48	28	22.0	23	2	Q71E75	HUMAN
49	28	22.0	23	2	Q7M3P0	DERPT
50	28	22.0	23	2	Q87082	9ALPH
51	28	22.0	23	2	Q87082	9ALPH
52	28	22.0	25	2	Q53174	RAT
53	28	22.0	26	2	Q6LCB3	MOUSE
54	28	22.0	26	2	Q8ESQ6	MOUSE
55	27.5	21.7	26	2	Q9NP34	HUMAN
56	27	21.3	13	2	Q9THS3	9CHLO
57	27	21.3	16	2	Q3YNF0	9DROME
58	27	21.3	16	2	Q95AY0	9ASTR
59	27	21.3	18	2	Q52RG6	HUMAN
60	27	21.3	18	2	Q6LD16	HUMAN
61	27	21.3	20	2	Q7M046	RAT
62	27	21.3	21	2	Q8CHC6	HUMAN
63	27	21.3	21	2	Q8Q2S9	CHICK
64	27	21.3	23	1	PRP1	RAT
65	27	21.3	23	2	Q49271	MYCGE
66	27	21.3	23	2	Q99162	9SMEG
67	27	21.3	24	2	Q4XFX5	PLACH
68	27	21.3	24	2	Q29403	SHEEP
69	27	21.3	24	2	Q4RDW1	TETNG
70	27	21.3	25	2	Q9UL44	HUMAN
71	27	21.3	26	2	Q7M319	PHOHI
72	26.5	20.9	20	2	Q9WSY4	9FLAV
73	26	20.5	10	2	Q9H3R9	HUMAN
74	26	20.5	10	2	Q71VN2	MOUSE
75	26	20.5	12	1	RR16	GINBI
76	26	20.5	13	2	Q56PI8	LACSA
77	26	20.5	14	2	Q6GWV6	SHEEP
78	26	20.5	15	2	Q4PZNC	ABUTH
79	26	20.5	15	2	Q8SLF5	9ASTR
80	26	20.5	15	2	Q8SLG7	9ASTR
81	26	20.5	16	2	Q4PZK7	DATST
82	26	20.5	16	2	Q05694	MOUSE
83	26	20.5	16	2	Q4PZK9	ACENE
84	26	20.5	16	2	Q4PZL7	9ERIC
85	26	20.5	16	2	Q4PZM7	PHYAM
86	26	20.5	16	2	Q4PZN5	9ROSI
87	26	20.5	16	2	Q4PZN8	9ASTR
88	26	20.5	16	2	Q4PZRE	9CARY
89	26	20.5	16	2	Q4PZS5	9ASTE
90	26	20.5	16	2	Q4PZS8	IMPFA
91	26	20.5	16	2	Q4PZS9	9ASTR
92	26	20.5	16	2	Q4PZT0	9ASTR
93	26	20.5	16	2	Q4PZT1	9ASTR
94	26	20.5	16	2	Q4PZT2	9ASTR
95	26	20.5	16	2	Q4PZT3	9ASTR
96	26	20.5	16	2	Q4PZT4	9ASTR
97	26	20.5	16	2	Q4PZT5	9ASTR
98	26	20.5	16	2	Q4PZT6	9ASTR
99	26	20.5	16	2	Q4PZT7	9ASTR
100	26	20.5	16	2	Q4PZT8	9ASTR

ALIGNMENTS

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